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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 04:10:42 ; Search time 1122.55 Seconds

(without alignments)  
10188.783 Million cell updates/sec

Title: US-09-963-803-19

Perfect score: 393

Sequence: 1 aagcttgatgcctgcagca.....cacacaactagagatcc 393

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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9: gb\_pr:\*  
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40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID        | Description        |
|------------|-------|-------------|--------|----|-----------|--------------------|
| 1          | 393   | 100.0       | 393    | 6  | AX036753  | AX036753 Sequence  |
| 2          | 314   | 79.9        | 462    | 6  | AX036754  | AX036754 Sequence  |
| 3          | 310   | 78.9        | 392    | 6  | AX036755  | AX036755 Sequence  |
| 4          | 304.6 | 77.5        | 600    | 6  | AX036756  | AX036756 Sequence  |
| 5          | 295.6 | 75.2        | 9285   | 6  | AX093047  | AX093047 Sequence  |
| 6          | 295.6 | 75.2        | 15077  | 6  | AX093052  | AX093052 Sequence  |
| 7          | 285.2 | 72.6        | 472    | 6  | AX036759  | AX036759 Sequence  |
| 8          | 214.4 | 54.6        | 317    | 6  | AX036737  | AX036737 Sequence  |
| 9          | 212.4 | 54.0        | 541    | 6  | AX036758  | AX036758 Sequence  |
| 10         | 200.4 | 51.0        | 348    | 6  | AX036757  | AX036757 Sequence  |
| 11         | 196.2 | 49.9        | 604    | 6  | AX036757  | AX036757 Sequence  |
| 12         | 154.8 | 39.4        | 371    | 6  | AX036739  | AX036739 Sequence  |
| 13         | 140.8 | 35.8        | 301    | 6  | AX036741  | AX036741 Sequence  |
| 14         | 140.8 | 35.8        | 398    | 6  | AX036740  | AX036740 Sequence  |
| 15         | 120.6 | 30.7        | 515    | 6  | AX036736  | AX036736 Sequence  |
| 16         | 120.6 | 30.7        | 515    | 6  | AX088388  | AX088388 Sequence  |
| 17         | 120.6 | 30.7        | 532    | 6  | AX0202413 | AX0202413 Sequence |
| 18         | 120.6 | 30.7        | 838    | 6  | AX014764  | AX014764 Sequence  |
| 19         | 120.6 | 30.7        | 853    | 6  | AX088389  | AX088389 Sequence  |
| 20         | 120.6 | 30.7        | 1036   | 6  | AX014765  | AX014765 Sequence  |
| 21         | 120.6 | 30.7        | 8159   | 14 | CVU20341  | CVU20341 Sequence  |
| 22         | 120.6 | 30.7        | 8159   | 14 | CVU59751  | CVU59751 Sequence  |
| 23         | 120.6 | 30.7        | 8340   | 6  | AX339231  | AX339231 Sequence  |
| 24         | 120.6 | 30.7        | 8340   | 6  | AX338536  | AX338536 Sequence  |
| 25         | 120.6 | 30.7        | 12241  | 6  | AX412168  | AX412168 Sequence  |
| 26         | 115.8 | 29.5        | 593    | 6  | AX088390  | AX088390 Sequence  |
| 27         | 115.8 | 29.5        | 857    | 6  | AX088391  | AX088391 Sequence  |
| 28         | 115.8 | 29.5        | 931    | 6  | AX088392  | AX088392 Sequence  |
| 29         | 115.4 | 29.4        | 931    | 6  | AX088393  | AX088393 Sequence  |
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| 31         | 81.4  | 20.7        | 7489   | 14 | CTWVC     | CTWVC Sequence     |
| 32         | 80    | 20.4        | 243    | 6  | AX036735  | AX036735 Sequence  |
| 33         | 77.8  | 19.8        | 392    | 6  | AX036755  | AX036755 Sequence  |
| 34         | 69.6  | 17.7        | 79     | 6  | AX036611  | AX036611 Sequence  |
| 35         | 69.6  | 17.7        | 79     | 6  | AX036748  | AX036748 Sequence  |
| 36         | 69    | 17.6        | 259    | 6  | AX036616  | AX036616 Sequence  |
| 37         | 69    | 17.6        | 296    | 6  | AX036603  | AX036603 Sequence  |
| 38         | 62    | 15.8        | 62     | 6  | AX036744  | AX036744 Sequence  |
| 39         | 62    | 15.3        | 60     | 6  | AX036743  | AX036743 Sequence  |
| 40         | 60    | 15.3        | 63     | 6  | AX036746  | AX036746 Sequence  |
| 41         | 58    | 14.8        | 80     | 6  | AX103782  | AX103782 Sequence  |
| 42         | 58    | 14.8        | 236    | 6  | AX103783  | AX103783 Sequence  |
| 43         | 58    | 14.8        | 299    | 6  | AX103784  | AX103784 Sequence  |
| 44         | 58    | 14.8        | 332    | 6  | AX103755  | AX103755 Sequence  |
| 45         | 58    | 14.8        | 472    | 6  | AX103753  | AX103753 Sequence  |

ALIGNMENTS

RESULT 1  
LOCUS AX036753 393 bp DNA linear PART 16-NOV-2000  
DEFINITION Sequence 19 from Patent WO0058485.  
ACCESSION AX036753  
VERSION AX036753.1 GI:11226262  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 393)  
AUTHORS Rance, I., Theisen, M. and Gruber, V.  
TITLE Chimeric expression promoters originating from commelina yellow  
mottle virus and Cassava vein mosaic virus  
JOURNAL Patent: WO 0058485-A 19 05-OCT-2000;

MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)  
FEATURES ; GRUBER VERONIQUE (FR)  
SOURCE location/Qualifiers  
1..393  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Promoter MPr1162"  
Promoter 1..393  
BASE COUNT 128 a 75 c 93 g 97 t  
ORIGIN

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Best Local Similarity 100.0%: Pred. No. 1.2e-102;  
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 61 GGAGATGAATAGCTAGCCATGACACTCTGTGGCAATATTGAAGACGTAGCAGCAG 120  
DB 61 GGAGATGAATAGCTAGCCATGACACTCTGTGGCAATATTGAAGACGTAGCAGCAG 120  
OY 121 AACATGAAAGAAAGAAAGTAAAGTCGCGTATGGAAGAGACATAGAGACATGTA 180  
DB 121 AACATGAAAGAAAGAAAGTAAAGTCGCGTATGGAAGAGACATAGAGACATGTA 180  
OY 181 AGGTGGAATAATGTAAGGGGGGAAAGTAACCTATGCTTATTTGGTTACGACTAGT 240  
DB 181 AGGTGGAATAATGTAAGGGGGGAAAGTAACCTATGCTTATTTGGTTACGACTAGT 240  
OY 241 GATTGATGTGATATCAAGATTGATGTATCTCCACTGACGTAAAGGATGACGATGCC 300  
DB 241 GATTGATGTGATATCAAGATTGATGTATCTCCACTGACGTAAAGGATGACGATGCC 300  
OY 301 ACGTTACCCGGTATCCCGTTCCCAAGCTTTATTTCTTATTTAAGCACTTGTAGTAG 360  
DB 301 ACGTTACCCGGTATCCCGTTCCCAAGCTTTATTTCTTATTTAAGCACTTGTAGTAG 360  
OY 361 CTTAGAAAACCAACACACACCTAGAGATCC 393  
DB 361 CTTAGAAAACCAACACACACCTAGAGATCC 393

RESULT 2  
AX036754 462 bp DNA Linear PAT 16-NOV-2000  
LOCUS AX036754  
DEFINITION Sequence 20 from Patent WO0058485.  
ACCESSION AX036754  
VERSION AX036754.1 GI:11226263  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 462)  
AUTHORS Rance, I., Theisen, M. and Gruber, V.  
TITLE Chimeric expression promoters originating from commelina yellow  
mottle virus and cassava vein mosaic virus  
JOURNAL Patent: WO 0058485-A 20 05-OCT-2000;  
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)  
FEATURES ; GRUBER VERONIQUE (FR)  
SOURCE location/Qualifiers  
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/db\_xref="taxon:32630"  
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Promoter 1..462  
BASE COUNT 148 a 87 c 111 g 116 t  
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Best Local Similarity 85.1%: Pred. No. 7.7e-80;  
Matches 393; Conservative 0; Mismatches 0; Indels 69; Gaps 1;

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OY 61 GGAGATGAATAGCTAGCCATGACACTCTGTGGCAATATTGAAGACGTAGCAGCAG 120  
DB 61 GGAGATGAATAGCTAGCCATGACACTCTGTGGCAATATTGAAGACGTAGCAGCAG 120  
OY 121 AACATGAAAGAAAGAAAGTAAAGTCGCGTATGGAAGAGACATAGAGACATGTA 180  
DB 121 AACATGAAAGAAAGAAAGTAAAGTCGCGTATGGAAGAGACATAGAGACATGTA 180  
OY 181 AGGTGGAATAATGTAAGGGGGGAAAGTAACCTATGCTTATTTGGTTACGACTAGT 240  
DB 181 AGGTGGAATAATGTAAGGGGGGAAAGTAACCTATGCTTATTTGGTTACGACTAGT 240  
OY 232 ----- 231  
DB 241 GATTGATGTGATATCAAGATTGATGTATCTCCACTGACGTAAAGGATGACGATGCC 300  
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DB 301 ACGACTAGTATGATGTATCAAGATTGATGTATCTCCACTGACGTAAAGGATG 360  
OY 292 ACGATGCCACGTTACCGGATGCGGTTCCCAAGCTTTATTTCTTATTTAAGCACTT 351  
DB 361 ACGATGCCACGTTACCGGATGCGGTTCCCAAGCTTTATTTCTTATTTAAGCACTT 420  
OY 352 GTGTAGTAGCTTAAAGAAACCAACACACACCTAGAGATCC 393  
DB 421 GTGTAGTAGCTTAAAGAAACCAACACACACCTAGAGATCC 462

RESULT 3  
AX036755 392 bp DNA Linear PAT 16-NOV-2000  
LOCUS AX036755  
DEFINITION Sequence 21 from Patent WO0058485.  
ACCESSION AX036755  
VERSION AX036755.1 GI:11226264  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 392)  
AUTHORS Rance, I., Theisen, M. and Gruber, V.  
TITLE Chimeric expression promoters originating from commelina yellow  
mottle virus and cassava vein mosaic virus  
JOURNAL Patent: WO 0058485-A 21 05-OCT-2000;  
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)  
FEATURES ; GRUBER VERONIQUE (FR)  
SOURCE location/Qualifiers  
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/organism="synthetic construct"  
/db\_xref="taxon:32630"  
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Promoter 1..392  
BASE COUNT 127 a 80 c 87 g 98 t  
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Query Match 78.9%: Score 310; DB 6; Length 392;  
Best Local Similarity 88.2%: Pred. No. 1.1e-78;  
Matches 337; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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DB 1 AAGCTTGATGCGCTGCAGACAGTATATCCGGCATCATGACATGACATGACTGTA 60  
OY 61 GGAGATGAATAGCTAGCCATGACACTCTGTGGCAATATTGAAGACGTAGCAGCAG 120  
DB 61 GGAGATGAATAGCTAGCCATGACACTCTGTGGCAATATTGAAGACGTAGCAGCAG 120  
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DB 121 AACATGAAAGAAAGAAAGTAAAGTCGCGTATGGAAGAGACATAGAGACATGTA 180

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Qy 181 AGGTGAAAAATGTAAGGCGGAAAGTAACCTTATGCAATTTGTTAGCAGTACT 240
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Db 181 AGGTGAAAAATGTAAGGCGGAAAGTAACCTTATGCAATTTGTTAGCAGTACT 240
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Qy 241 GATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATGACCATGCC 300
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Db 241 GCGTCATCCCTTACGTAGTGAGATATACATCAATCTTGATATCAATCAATCCACTAG 300
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Qy 301 ACCTTACCCGGTATGCCGGTCCCAAGCTTATTTCCCTTATTTAAGACATGTTAGTAG 360
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Db 301 TCGTTACCCGGTATGCCGGTCCCAAGCTTATTTCCCTTATTTAAGCATTGTGTAGTAG 360
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Qy 361 CTTAGAAAAACCAACAACAAC 382
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Db 361 CTTAGAAAAACCAACAACAAC 382
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RESULT 4
LOCUS AX036756 600 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 22 from Patent WO0058485.
ACCESSION AX036756
VERSION AX036756.1 GI:11226265
KEYWORDS
SOURCE .
ORGANISM synthetic construct.
artificial sequences.
REFERENCE 1 (bases 1 to 600)
AUTHORS Rance,I., Theisen,M. and Gruber,V.
TITLE Chimeric expression promoters originating from commelina yellow
JOURNAL mottle virus and cassava vein mosaic virus
PATENT: WO 0058485-A 22 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
FEATURES
location/Qualifiers
source 1..600
/organism="synthetic construct"
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promoter 1..600
BASE COUNT 188 a 111 c 147 g 154 t
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Best Local Similarity 94.3%; Pred. No. 4e-77;
Matches 316; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
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RESULT 5
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DEFINITION Sequence 52 from Patent WO0118192.
ACCESSION AX093047
VERSION AX093047.1 GI:13509522
KEYWORDS
SOURCE .
ORGANISM synthetic construct.
artificial sequences.
REFERENCE 1 (bases 1 to 9285)
AUTHORS Gruber,V. and Comeau,D.
TITLE Synthetic vectors, transgenic plants containing them, and methods
JOURNAL for obtaining them
PATENT: WO 0118192-A 52 15-MAR-2001;
MERISTEM THERAPEUTICS (FR)
FEATURES
location/Qualifiers
source 1..9285
/organism="synthetic construct"
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/note="PMRT1336"
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ORIGIN

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Best Local Similarity 94.2%; Pred. No. 1.0e-74;
Matches 307; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Db 5799 TGCCTGAGCAGCTAGTATCCGCCGTCATCATGACATCATCAGTACTGAGAGATGAA 5858
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Qy 70 TAGCTAGCAGTACACTCTGTGCAATTTGGAAGACGTAAAGCAGTACGACACATGAA 129
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Db 5859 TAGCTAGCAGTACACTCTGTGCAATTTGGAAGACGTAAAGCAGTACGACACATGAA 5918
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Qy 130 AAGAAGAAATAGAGTGGGATGTGGAAGAGACATGAGAGACATGTAAGGTGAAA 189
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Db 5919 AAGAAGAAATAGAGTGGGATGTGGAAGAGACATGAGAGACATGTAAGGTGAAA 5978
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Qy 190 ATGTAAGGCGGAAAGTAACCTTATGCAATTTGTAATTTGTTAGCAGTATGATGAT 249
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Db 5979 ATGTAAGGCGGAAAGTAACCTTATGCAATTTGTAATTTGTTAGCAGTATGATGAT 6038
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Qy 250 GATATCAAGATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCAGTTAACC 309
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Db 6039 GATATCAAGATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCAGTTAAGT 6098
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Qy 310 GGTATGCCGGTCCCAAGCTTATTT 335
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Db 6099 GATTGATGTGATATCAAGATTGATGT 6124
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RESULT 6
LOCUS AX093052 15077 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 57 from Patent WO0118192.
ACCESSION AX093052
VERSION AX093052.1 GI:13509527
KEYWORDS
SOURCE .
ORGANISM synthetic construct.
artificial sequences.
REFERENCE 1 (bases 1 to 15077)
AUTHORS Gruber,V. and Comeau,D.
TITLE Synthetic vectors, transgenic plants containing them, and methods
for obtaining them
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Db 227 -----|||||  
GTACCAGTATGCCG 243

Qy 320 TTCCCAAGCTTATTTCTTATTTAGACACTTGTGTAGTACTTATAGAAACCAACACAC 379  
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Db 244 TTCCCAAGCTTATTTCTTATTTAGACACTTGTGTAGTACTTATAGAAACCAACACAC 303  
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Qy 380 AACCTAGAGATCC 393  
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Db 304 AACCTAGAGATCC 317

RESULT 9  
AX036758 541 bp DNA linear PAT 16-NOV-2000  
LOCUS  
DEFINITION Sequence 24 from Patent W00058485.  
ACCESSION AX036758  
VERSION AX036758.1 GI:11226267  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM  
REFERENCE 1 (bases 1 to 541)  
AUTHORS Rance,I., Theisen,M. and Gruber,V.  
TITLE Chimeric expression promoters originating from commelina yellow  
mottle virus and cassava vein mosaic virus  
PATENT: WO 0058485-A 24 05-OCT-2000;  
JOURNAL MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)  
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Location/Qualifiers  
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Promoter 1..541  
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Matches 236; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

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Db 160 CATGCCACTGTGCGAATATTGAAGACGTAGACAGTGAACAACATGAAGAAGAA 219  
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Qy 138 GATAAGTCGGTGTATTTGAAGAAGACATAGAGACACATGTAAGTGAAGTGAAG 197  
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Db 220 GATAAGTCGGTGTATTTGAAGAAGACATAGAGACACATGTAAGTGAAGTGAAG 278  
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Qy 198 GCGGAAGTAACTTATGATTTGTAATTGCTTACGACTAGTGAATGATGATATCA 257  
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Db 279 GCGGAAGTAACTTATGATTTGTAATTGCTTACGACTAGTGAATGATGATATCA 338  
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Qy 258 GATGATGTGATATCTCCAGTGAAGGATGACGATGACGATGACGATGACGATGAC 317  
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Db 339 GATGATGTGATATCTCCAGTGAAGGATGACGATGACGATGACGATGACGATGAC 398  
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Qy 318 GGTTCACCAAGCTTATTT 335  
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Db 399 TGATATCAAGATGATGT 416

RESULT 10  
AX036738 348 bp DNA linear PAT 16-NOV-2000  
LOCUS  
DEFINITION Sequence 4 from Patent W00058485.  
ACCESSION AX036738  
VERSION AX036738.1 GI:11226247  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM  
artificial sequences.

REFERENCE 1 (bases 1 to 348)  
AUTHORS Rance,I., Theisen,M. and Gruber,V.  
TITLE Chimeric expression promoters originating from commelina yellow  
mottle virus and cassava vein mosaic virus  
PATENT: WO 0058485-A 4 05-OCT-2000;  
JOURNAL MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)  
FEATURES  
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Location/Qualifiers  
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/note="promoter MPr1117"

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Best Local Similarity 99.1%; Pred. No. 4.9e-47;  
Matches 212; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Db 52 ACTAGTATCCCGCTCATCATATGACATCATCATCATCATCATCATCATCATCATCAT 111  
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Qy 80 TGACACTGTGCGAATATTGAAGACGTAGACAGTGAACAACATGAAGAAGAA 139  
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Db 112 TGACACTGTGCGAATATTGAAGACGTAGACAGTGAACAACATGAAGAAGAA 171  
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Qy 140 TAAAGTCGTGATTTGTGAAGAAGACATAGAGACATGTAAGTGAAGTGAAGTGAAG 199  
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Db 172 TAAAGTCGTGATTTGTG- AAGAGACATAGAGACATGTAAGTGAAGTGAAGTGAAG 230  
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Qy 200 GGAAGTAACTTATGATTTGTAATTGCTTAC 233  
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Db 231 GGAAGTAACTTATGATTTGTAATTGCTTAC 264  
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RESULT 11  
AX036757 604 bp DNA linear PAT 16-NOV-2000  
LOCUS  
DEFINITION Sequence 23 from Patent W00058485.  
ACCESSION AX036757  
VERSION AX036757.1 GI:11226266  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM  
REFERENCE 1 (bases 1 to 604)  
AUTHORS Rance,I., Theisen,M. and Gruber,V.  
TITLE Chimeric expression promoters originating from commelina yellow  
mottle virus and cassava vein mosaic virus  
PATENT: WO 0058485-A 23 05-OCT-2000;  
JOURNAL MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)  
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Location/Qualifiers  
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Promoter 1..604  
BASE COUNT 186 a 116 c 145 g 157 t  
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Db      279 GCGGAAGTAACCTTATGATTTGTAATTTGGTTAC-CTAGATTTGATGATATCA 336
Oy      258 GATTGATGATATCTCCACTGACGTAGAGATGACGATGCCAGCT 304
Db      337 GATTGATGATATCTCCACTGACGTAGAGATGACGATGCCAGCT 383

RESULT 12
AX036739          371 bp      DNA      linear      PAT 16-NOV-2000
LOCUS             AX036739
DEFINITION        Sequence 5 from Patent W0058485.
ACCESSION          AX036739
VERSION            AX036739.1 GI:11226248
KEYWORDS
SOURCE             synthetic construct.
ORGANISM           synthetic construct.
REFERENCE           1 (bases 1 to 371)
AUTHORS            Range,I., Theisen,M. and Gruber,Y.
TITLE              Chimeric expression promoters originating from commelina yellow
JOURNAL            mottle virus and cassava vein mosaic virus
                   Patent: WO 0058485-A 5 05-OCT-2000;
                   MERISTEM THERAPEUTICS (FR) ; RANCE INNN (FR) ; THEISEN MANFRED (FR)
FEATURES
   source           location/Qualifiers
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BASE COUNT         122 a      68 c      89 g      92 t
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Query Match        39.4%; Score 154.8; DB 6; Length 371;
Best Local Similarity 75.9%; Pred. No. 7.3e-34;
Matches 240; Conservative 0; Mismatches 2; Indels 74; Gaps 1;

Oy      78 CATGACACTCTGTGCGAATATTGAAGACGTAGACGACACAAATGAAAGAA 137
Db      130 CATGCCACTCTGTGCGAATATTGAAGACGTAGACGACACAAATGAAAGAA 189
Oy      138 GATTAAGTCGTGATTGTGTAAGAGACATAGAGACATGTAAGGTGGAATAATGTAAG 197
Db      190 GATTAAGTCGTGATTGTGTAAGAGACATAGAGACATGTAAGGTGGAATAATGTAAG 249
Oy      198 GCGGAAGTAACCTTATGATTTGTAATTTGGTTACGATGATTGATATCA 257
Db      250 GCGGAAGTAACCTTATGATTTGTAATTTGGTTACGATGATTGATATCA 280
Oy      258 GATTGATGATATCTCCACTGACGTAGAGATGACGATGCCAGCTTACCCGATGCC 317
Db      281 -----CTTACCCGATGCC 295
Oy      318 GATTCCCAAGCTTATTTCTTATTAAGCACTTGTGTAGTACTTGAAGAAACCAACACA 377
Db      296 GATTCCCAAGCTTATTTCTTATTAAGCACTTGTGTAGTACTTGAAGAAACCAACACA 355
Oy      378 ACAACCTAGAGATCC 393
Db      356 ACAACCTAGAGATCC 371

RESULT 13
AX036741          301 bp      DNA      linear      PAT 16-NOV-2000
LOCUS             AX036741
DEFINITION        Sequence 7 from Patent W0058485.
ACCESSION          AX036741
VERSION            AX036741.1 GI:11226250
KEYWORDS

```

```

SOURCE             synthetic construct.
ORGANISM           synthetic construct.
REFERENCE           1 (bases 1 to 301)
AUTHORS            Range,I., Theisen,M. and Gruber,Y.
TITLE              Chimeric expression promoters originating from commelina yellow
JOURNAL            mottle virus and cassava vein mosaic virus
                   Patent: WO 0058485-A 7 05-OCT-2000;
                   MERISTEM THERAPEUTICS (FR) ; RANCE INNN (FR) ; THEISEN MANFRED (FR)
FEATURES
   source           location/Qualifiers
                   1..301
                   /organism="synthetic construct"
                   /db_xref="taxon:32630"
                   /note="promoter Mpr1154"
BASE COUNT         98 a      54 c      74 g      75 t
ORIGIN
Query Match        35.8%; Score 140.8; DB 6; Length 301;
Best Local Similarity 98.1%; Pred. No. 8.1e-30;
Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Oy      78 CATGACACTCTGTGCGAATATTGAAGACGTAGACGACACAAATGAAAGAA 137
Db      63 CATGCCACTCTGTGCGAATATTGAAGACGTAGACGACACAAATGAAAGAA 122
Oy      138 GATTAAGTCGTGATTGTGTAAGAGACATAGAGACATGTAAGGTGGAATAATGTAAG 197
Db      123 GATTAAGTCGTGATTGTGTAAGAGACATAGAGACATGTAAGGTGGAATAATGTAAG 181
Oy      198 GCGGAAGTAACCTTATGATTTGTAATTTGGTTAC 233
Db      182 GCGGAAGTAACCTTATGATTTGTAATTTGGTTAC 217

RESULT 14
AX036740          398 bp      DNA      linear      PAT 16-NOV-2000
LOCUS             AX036740
DEFINITION        Sequence 6 from Patent W0058485.
ACCESSION          AX036740
VERSION            AX036740.1 GI:11226249
KEYWORDS
SOURCE             synthetic construct.
ORGANISM           synthetic construct.
REFERENCE           1 (bases 1 to 398)
AUTHORS            Range,I., Theisen,M. and Gruber,Y.
TITLE              Chimeric expression promoters originating from commelina yellow
JOURNAL            mottle virus and cassava vein mosaic virus
                   Patent: WO 0058485-A 6 05-OCT-2000;
                   MERISTEM THERAPEUTICS (FR) ; RANCE INNN (FR) ; THEISEN MANFRED (FR)
FEATURES
   source           location/Qualifiers
                   1..398
                   /organism="synthetic construct"
                   /db_xref="taxon:32630"
                   /note="promoter Mpr1147"
BASE COUNT         128 a      80 c      93 g      97 t
ORIGIN
Query Match        35.8%; Score 140.8; DB 6; Length 398;
Best Local Similarity 98.1%; Pred. No. 8.1e-30;
Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Oy      78 CATGACACTCTGTGCGAATATTGAAGACGTAGACGACACAAATGAAAGAA 137
Db      160 CATGCCACTCTGTGCGAATATTGAAGACGTAGACGACACAAATGAAAGAA 219
Oy      138 GATTAAGTCGTGATTGTGTAAGAGACATAGAGACATGTAAGGTGGAATAATGTAAG 197
Db      220 GATTAAGTCGTGATTGTG-AAGAGACATAGAGACATGTAAGGTGGAATAATGTAAG 278

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OY 198 GCGGAAGTAACCTTATCATTTGTAATTGTTAC 233  
 ||||||||||||||||||||||||||||||||  
 Db 279 GCGGAAGTAACCTTATCATTTGTAATTGTTAC 314

## RESULT 15

AX036736

LOCUS AX036736 515 bp DNA linear PAT 16-NOV-2000

DEFINITION Sequence 2 from Patent WO058485.

ACCESSION AX036736

VERSION AX036736.1 GI:11226245

KEYWORDS

SOURCE synthetic construct.

ORGANISM synthetic construct.

REFERENCE 1 (bases 1 to 515)

AUTHORS Rance, I., Theisen, M. and Gruber, V.

TITLE Chimeric expression promoters originating from commelina yellow

JOURNAL mottle virus and cassava vein mosaic virus

PATENT: WO 0058485-A 2 05-OCT-2000.

MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)

; GRUBER VERONIQUE (FR)

FEATURES

source location/Qualifiers

1..515 /organism="synthetic construct"

/db\_xref="taxon:32630"

/note="Promoter from the intergenic region of Cassava Vein

Mosaic Virus of 515 bp in length EMBL U59751"

promoter

BASE COUNT 198 a 79 c 109 g 129 t

ORIGIN

Query Match 30.7%; Score 120.6; DB 6; Length 515;  
 Best Local Similarity 93.3%; Pred. No. 5.5e-24;  
 Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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 |||||

Db 216 GAATCTTGAAAGACGTAGACACTGACGACAAATGAAAGAGAGATAAGTGTGAT 275  
 |||||

OY 153 TGTGAAGAGACATAGACACATGTAGGTGGAATGTAAAGCGCGAAAGTAACCTT 212  
 |||||

Db 276 TGTGAAGAGACATAGACACATGTAGGTGGAATGTAAAGCGCGCGAAAGTAACCTT 335  
 |||||

OY 213 ATGCATTGTAAATT 227  
 |||

Db 336 ATCACAAGGAATCT 350  
 |||

Search completed: April 14, 2003, 09:29:14  
 Job time : 1133.55 secs



GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 04:03:41 ; Search time 126.948 Seconds

(without alignments)  
6971.612 Million cell updates/sec

Title: us-09-963-803-19

Perfect score: 393

Sequence: 1 aagctgcatacctgcagca.....cacacaactagagatcc 393

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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| 1          | 393   | 100.0       | 393    | 21    | AAA96853    |
| 2          | 314   | 79.9        | 462    | 21    | AAA96854    |
| 3          | 310   | 78.9        | 392    | 21    | AAA96855    |
| 4          | 304.6 | 77.5        | 600    | 21    | AAA96856    |
| 5          | 285.2 | 72.6        | 472    | 21    | AAA96859    |
| 6          | 214.4 | 54.6        | 317    | 21    | AAA96837    |
| 7          | 212.4 | 54.0        | 341    | 21    | AAA96858    |
| 8          | 200.4 | 51.0        | 348    | 21    | AAA96838    |
| 9          | 196.2 | 49.9        | 604    | 21    | AAA96857    |

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|----|-------|------|-------|----|-----------|---------------------|
| 10 | 154.8 | 39.4 | 371   | 21 | AAA96839  | Nucleotide sequenc  |
| 11 | 140.8 | 35.8 | 301   | 21 | AAA96841  | Nucleotide sequenc  |
| 12 | 140.8 | 35.8 | 398   | 21 | AAA96840  | Nucleotide sequenc  |
| 13 | 120.6 | 30.7 | 392   | 19 | AAV14019  | CSVMV promoter CVP  |
| 14 | 120.6 | 30.7 | 411   | 19 | AAV14021  | CSVMV promoter pb.  |
| 15 | 120.6 | 30.7 | 515   | 21 | AAA96836  | Promoter from inte  |
| 16 | 120.6 | 30.7 | 515   | 22 | AAFE5505  | Nucleotide sequenc  |
| 17 | 120.6 | 30.7 | 524   | 19 | AAV14020  | CSVMV promoter CVP  |
| 18 | 120.6 | 30.7 | 526   | 19 | AAV14018  | CSVMV promoter pa.  |
| 19 | 120.6 | 30.7 | 532   | 22 | AAAD11575 | Cassava vein Mosaic |
| 20 | 120.6 | 30.7 | 853   | 22 | AAFE5506  | Nucleotide sequenc  |
| 21 | 120.6 | 30.7 | 1839  | 24 | ABL57988  | 4-Hydroxyphenylpyr  |
| 22 | 120.6 | 30.7 | 4677  | 24 | ABL57989  | 4-Hydroxyphenylpyr  |
| 23 | 120.6 | 30.7 | 8187  | 24 | ABL58082  | Binary vector pAG1  |
| 24 | 120.6 | 30.7 | 8340  | 24 | ABA04755  | Binary vector pAG1  |
| 25 | 120.6 | 30.7 | 8340  | 24 | ABD04139  | Tomato anthocyanin  |
| 26 | 120.6 | 30.7 | 12241 | 24 | ABO73049  | Binary vector DNA   |
| 27 | 120.6 | 30.7 | 12241 | 24 | ABD36732  | CSVMV promoter pc.  |
| 28 | 117.4 | 29.9 | 305   | 19 | AAV14022  | CSVMV promoter pde  |
| 29 | 117.4 | 29.9 | 420   | 19 | AAV14026  | CSVMV promoter. C   |
| 30 | 117   | 29.8 | 476   | 19 | AAV14053  | Nucleotide sequenc  |
| 31 | 115.8 | 29.5 | 593   | 22 | AAFE5507  | Nucleotide sequenc  |
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| 35 | 115.4 | 29.4 | 931   | 22 | AAFE5510  | Nucleotide sequenc  |
| 36 | 81.8  | 20.8 | 482   | 19 | AAV14027  | CSVMV promoter pde  |
| 37 | 81    | 20.6 | 441   | 19 | AAV14033  | Promoter from inte  |
| 38 | 80    | 20.4 | 243   | 21 | AAA96835  | CSVMV promoter pde  |
| 39 | 79.6  | 20.3 | 491   | 19 | AAV14030  | CSVMV promoter pde  |
| 40 | 77.8  | 19.8 | 392   | 21 | AAA96855  | Nucleotide sequenc  |
| 41 | 77.4  | 18.8 | 261   | 19 | AAV14023  | CSVMV promoter pd.  |
| 42 | 69.6  | 17.7 | 79    | 21 | AAA96848  | Directional desoxy  |
| 43 | 69.6  | 17.7 | 79    | 21 | AAA96472  | Nucleotide sequenc  |
| 44 | 69    | 17.6 | 259   | 21 | AAA96477  | Nucleotide sequenc  |
| 45 | 69    | 17.6 | 296   | 21 | AAA96465  | Nucleotide sequenc  |

## ALIGNMENTS

RESULT 1

AAA96853

ID AAA96853 standard; DNA; 393 BP.

XX

AC AAA96853;

XX

DT 19-FEB-2001 (first entry)

XX

DE Nucleotide sequence of chimeric expression promoter Mp1162.

XX

KW Promoter; Intergenic region; Commelina yellow mottle virus;

KW chimeric expression promoter; plant vascular expression promoter;

KM plant green tissue expression promoter; Cassava vein mosaic virus;

KM transgenic plant; chimera; ss.

XX

OS Chimeric - Commelina yellow mottle virus.

OS Chimeric - Cassava vein mosaic virus.

XX

PN WO200058485-A1.

XX

PD 05-OCT-2000.

XX

PF 29-MAR-2000; 2000WO-IB00370.

XX

PR 29-MAR-1999; 99FR-0003925.

XX

PA (MERI-) MERISTEM THERAPEUTICS.

XX

PI Rance I, Gruber V, Theisen M;

XX

DR WPI: 2000-647238/62.

PT Chimeric expression promoter for transgenic plant production, comprises  
PT sequence from promoter comprising vascular expression region replaced  
PT with sequence from promoter comprising green tissue expression region  
XX  
XX  
PS Claim 5; Page 85; 91pp; English.  
XX  
XX The present sequence represents a chimeric promoter of the invention.  
CC The specification describes chimeric expression promoters. These  
CC chimeric promoters comprise a nucleic acid sequence which is derived  
CC from a first plant promoter, in which a plant vascular expression  
CC promoter region is replaced with a nucleic acid sequence derived from  
CC a second plant promoter comprising a plant green tissue expression  
CC promoter region. Preferably, the first plant promoter originates from  
CC Commelina yellow mottle virus, and the second plant promoter originates  
CC from the Cassava vein mosaic virus. Especially, the promoters are  
CC derived from intergenic regions. The chimeric promoters are useful  
CC for producing transgenic plants.  
XX  
XX  
SQ Sequence 393 BP; 128 A; 75 C; 93 G; 97 T; 0 other;  
XX  
XX  
Query Match 100.0%; Score 393; DB 21; Length 393;  
Best Local Similarity 100.0%; Pred. No. 8e-111;  
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 AACCTTGCAATGCTCGAGCACTAGTATCCGCCGTCAATGACATCATCAGTACTGA 60  
DB 1 AACCTTGCAATGCTCGAGCACTAGTATCCGCCGTCAATGACATCATCAGTACTGA 60  
OY 61 GGAGATGAATAGCTAGACACTGCTGTGGCAATTTGAGAGAGTAAAGCACTGACGAC 120  
DB 61 GGAGATGAATAGCTAGACACTGCTGTGGCAATTTGAGAGAGTAAAGCACTGACGAC 120  
OY 121 AACATGAAAGAAAGATAGTGTGATGTGAAGAGACATAGAGACATGTA 180  
DB 121 AACATGAAAGAAAGATAGTGTGATGTGAAGAGACATAGAGACATGTA 180  
OY 181 AGGTGAAATATGTAAGGGGGAAGTAACTTATGCAATTTGTAATTTGGTTACGACTAGT 240  
DB 181 AGGTGAAATATGTAAGGGGGAAGTAACTTATGCAATTTGTAATTTGGTTACGACTAGT 240  
OY 241 GATTGATGTGATATCAAGATTTGATATCTCCACTGACGTAAGGATGACGATGCC 300  
DB 241 GATTGATGTGATATCAAGATTTGATATCTCCACTGACGTAAGGATGACGATGCC 300  
OY 301 ACCTTACCGGATGCGCGGTTCCCAAGCTTATTTCTTATTTAAGCAGCTGTGTAGT 360  
DB 301 ACCTTACCGGATGCGCGGTTCCCAAGCTTATTTCTTATTTAAGCAGCTGTGTAGT 360  
OY 361 CTTAGAAACCAACACACAACTAGAGATCC 393  
DB 361 CTTAGAAACCAACACACAACTAGAGATCC 393  
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XX  
XX  
AC AAA96854;  
XX  
XX 19-FEB-2001 (first entry)  
XX  
XX Nucleotide sequence of chimeric expression promoter MP1163.  
DE Promoter; intergenic region; Commelina yellow mottle virus;  
XX chimeric expression promoter; plant vascular expression promoter;  
KM plant green tissue expression promoter; Cassava vein mosaic virus;  
KM transgenic plant; chimera; ss.  
XX  
XX Chimeric - Commelina yellow mottle virus.  
OS Chimeric - Cassava vein mosaic virus.  
XX  
XX WO200056485-A1.  
PN

XX  
PD 05-OCT-2000.  
XX  
XX 29-MAR-2000; 2000MO-1B00370.  
PF  
XX  
PR 29-MAR-1999; 99PR-0003925.  
XX  
XX (MERI-) MERISTEM THERAPEUTICS.  
XX  
XX Range I, Gruber V, Theisen M;  
XX  
XX WPI; 2000-647238/62.  
DR  
XX  
XX Chimeric expression promoter for transgenic plant production, comprises  
PT sequence from promoter comprising vascular expression region replaced  
PT with sequence from promoter comprising green tissue expression region  
XX  
XX  
PS Claim 5; Page 86; 91pp; English.  
XX  
XX  
XX The present sequence represents a chimeric promoter of the invention.  
CC The specification describes chimeric expression promoters. These  
CC chimeric promoters comprise a nucleic acid sequence which is derived  
CC from a first plant promoter, in which a plant vascular expression  
CC promoter region is replaced with a nucleic acid sequence derived from  
CC a second plant promoter comprising a plant green tissue expression  
CC promoter region. Preferably, the first plant promoter originates from  
CC Commelina yellow mottle virus, and the second plant promoter originates  
CC from the Cassava vein mosaic virus. Especially, the promoters are  
CC derived from intergenic regions. The chimeric promoters are useful  
CC for producing transgenic plants.  
XX  
XX  
SQ Sequence 462 BP; 148 A; 87 C; 111 G; 116 T; 0 other;  
XX  
XX  
Query Match 79.9%; Score 314; DB 21; Length 462;  
Best Local Similarity 85.1%; Pred. No. 1.7e-86;  
Matches 393; Conservative 0; Mismatches 0; Indels 69; Gaps 1;  
OY 1 AACCTTGCAATGCTCGAGCACTAGTATCCGCCGTCAATGACATCATCAGTACTGA 60  
DB 1 AACCTTGCAATGCTCGAGCACTAGTATCCGCCGTCAATGACATCATCAGTACTGA 60  
OY 61 GGAGATGAATAGCTAGACACTGCTGTGGCAATTTGAGAGAGTAAAGCACTGACGAC 120  
DB 61 GGAGATGAATAGCTAGACACTGCTGTGGCAATTTGAGAGAGTAAAGCACTGACGAC 120  
OY 121 AACATGAAAGAAAGATAGTGTGATGTGAAGAGACATAGAGACATGTA 180  
DB 121 AACATGAAAGAAAGATAGTGTGATGTGAAGAGACATAGAGACATGTA 180  
OY 181 AGGTGAAATATGTAAGGGGGAAGTAACTTATGCAATTTGTAATTTGGTTACGACTAGT 240  
DB 181 AGGTGAAATATGTAAGGGGGAAGTAACTTATGCAATTTGTAATTTGGTTACGACTAGT 240  
OY 232 ----- 231  
DB 241 GATTGATGTGATATCAAGATTTGATATCTCCACTGACGTAAGGATGACGATGCC 300  
OY 232 ACAGCTAGATGATGATATCAAGATTTGATATCTCCACTGACGTAAGGATG 291  
DB 301 ACAGCTAGATGATGATATCAAGATTTGATATCTCCACTGACGTAAGGATG 360  
OY 292 ACAGCTAGATGATGATATCAAGATTTGATATCTCCACTGACGTAAGGATG 351  
DB 361 ACAGCTAGATGATGATATCAAGATTTGATATCTCCACTGACGTAAGGATG 420  
OY 352 GTGTAGTACTTAGAAACCAACACAACTAGAGATCC 393  
DB 421 GTGTAGTACTTAGAAACCAACACAACTAGAGATCC 462  
RESULT 3  
AA96855

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ID AAA96855 standard; DNA; 392 BP.
XX
AC AAA96855:
XX
DT 19-FEB-2001 (first entry)
XX
DE Nucleotide sequence of chimeric expression promoter Mp1164.
XX
KW Promoter; intergenic region; Commelina yellow mottle virus;
KW chimeric expression promoter; plant vascular expression promoter;
KW plant green tissue expression promoter; Cassava vein mosaic virus;
KW transgenic plant; chimera; ss.
XX
OS Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
PN WO200058485-A1.
XX
PD 05-OCT-2000.
XX
PF 29-MAR-2000; 2000WO-IB00370.
XX
PR 29-MAR-1999; 99FR-0003925.
XX
PA (MERI-) MERISTEM THERAPEUTICS.
XX
PI Rance I, Gruber V, Theisen M;
XX
DR WPI; 2000-647238/62.
XX
PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
PS Claim 5; Page 86; 91pp; English.
XX
CC The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 392 BP; 127 A; 80 C; 87 G; 98 T; 0 other:
Query Match 78.9%; Score 310; DB 21; Length 392;
Best Local Similarity 88.2%; Pred. No. 2.6e-85;
Matches 337; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
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DB 1 AAGCTGCATCCTGCAGCACTAGTATCGCGTCATCAATGACATCATCTACAGTACTGA 60
OY 61 GGAGATGAATAGTACGACATGACACTCTGTGCGAATATTTGAAGACGTAAAGCACTGACGAC 120
DB 61 GGAGATGAATAGTACGACATGACACTCTGTGCGAATATTTGAAGACGTAAAGCACTGACGAC 120
OY 121 AACATGAAAAAGAGAGATAGTGGTGTGTTGTAAGAGACATAGAGACACATGTA 180
DB 121 AACATGAAAAAGAGAGATAGTGGTGTGTTGTAAGAGACATAGAGACACATGTA 180
OY 181 AGGTGAAAAATGTAAGGCGGAAGTAACCTTATGCAATTTGTGTTACGACTAGT 240
DB 181 AGGTGAAAAATGTAAGGCGGAAGTAACCTTATGCAATTTGTGTTACGACTAGT 240
OY 241 GATTGATGTGATATCAAGATGATGTGATATCTCCACTGACGTAAAGGATGACCATGCC 300
DB 241 GATTGATGTGATATCAAGATGATGTGATATCTCCACTGACGTAAAGGATGACCATGCC 300
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DB 241 GCGTATCCCTTACGTCAGTGGAGATATCATCATCTGTGATATACATCATCACTAG 300
OY 301 ACGTTACCCGGGTATGCCGGTTCCTTATTTTAAAGACCTTGCTAGTAG 360
DB 301 TCGTTACCCGGGTATGCCGGTTCCTTATTTTAAAGACCTTGCTAGTAG 360
OY 361 CTTAGAAAAACACACACACAC 382
DB 361 CTTAGAAAAACACACACACAC 382
RESULT 4
ID AAA96856 standard; DNA; 600 BP.
XX
AC AAA96856:
XX
DT 19-FEB-2001 (first entry)
XX
DE Nucleotide sequence of chimeric expression promoter Mp1165.
XX
KW Promoter; intergenic region; Commelina yellow mottle virus;
KW chimeric expression promoter; plant vascular expression promoter;
KW plant green tissue expression promoter; Cassava vein mosaic virus;
KW transgenic plant; chimera; ss.
XX
OS Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
PN WO200058485-A1.
XX
PD 05-OCT-2000.
XX
PF 29-MAR-2000; 2000WO-IB00370.
XX
PR 29-MAR-1999; 99FR-0003925.
XX
PA (MERI-) MERISTEM THERAPEUTICS.
XX
PI Rance I, Gruber V, Theisen M;
XX
DR WPI; 2000-647238/62.
XX
PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
PS Claim 5; Page 86-87; 91pp; English.
XX
CC The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 600 BP; 188 A; 111 C; 147 G; 154 T; 0 other:
Query Match 77.5%; Score 304.6; DB 21; Length 600;
Best Local Similarity 94.3%; Pred. No. 1.4e-83;
Matches 316; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
OY 1 AAGCTGCATCCTGCAGCACTAGTATCGCGTCATCAATGACATCATCACTAGTACTGA 60
DB 1 AAGCTGCATCCTGCAGCACTAGTATCGCGTCATCAATGACATCATCACTAGTACTGA 60
OY 61 GGAGATGAATAGTACGACATGACACTCTGTGCGAATATTTGAAGACGTAAAGCACTGACGAC 120
```

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|||||
Db 61 GGAGATAGTACCTACCTGACACTCTGCGAATATTGAMAGCGTAACGCTAGCAGAC 120
OY 121 AACAATGAAAGAAGAAAGTAAAGTCGTGATGTGAAGAAGACATAGAGACAACTGTA 180
Db 121 AACAATGAAAGAAGAAAGTAAAGTCGTGATGTGAAGAAGACATAGAGACAACTGTA 180
OY 181 AGGTGGAATATGTAAGGCGGGAAGTAACTTATGCAATTTGTAATTTGTTAGCACTAGT 240
Db 181 AGGTGGAATATGTAAGGCGGGAAGTAACTTATGCAATTTGTAATTTGTTAGCACTAGT 240
OY 241 GATTGATGTGATATCAAGATTTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCC 300
Db 241 GATTGATGTGATATCAAGATTTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCC 300
OY 301 ACCTTACCGCGTATGCCGCTTCCCAAGCTTATTT 335
Db 301 ACCTTACCGCGTATGCCGCTTCCCAAGCTTATTT 335
```

RESULT 5  
AAA96859

ID AAA96859 standard; DNA; 472 BP.

AC AAA96859;

DT 19-FEB-2001 (first entry)

DE Nucleotide sequence of chimeric expression promoter MP1169.

KW Promoter; intergenic region; Commelina yellow mottle virus;

KW chimeric expression promoter; plant vascular expression promoter;

KW plant green tissue expression promoter; Cassava vein mosaic virus;

KW transgenic plant; chimera; ss.

OS Chimeric - Commelina yellow mottle virus.

OS Chimeric - Cassava vein mosaic virus.

PN WO200058485-A1.

PD 05-OCT-2000.

PF 29-MAR-2000; 2000MO-IB00370.

PR 29-MAR-1999; 99FR-0003925.

PA (MERI-) MERISTEM THERAPEUTICS.

PI Rance I, Gruber V, Theisen M;

PI Rance I, Gruber V, Theisen M;

PI Rance I, Gruber V, Theisen M;

PI Rance I, Gruber V, Theisen M;

PI Rance I, Gruber V, Theisen M;

PI Rance I, Gruber V, Theisen M;

PI Rance I, Gruber V, Theisen M;

PI Rance I, Gruber V, Theisen M;

PI Rance I, Gruber V, Theisen M;

PI Rance I, Gruber V, Theisen M;

PI Rance I, Gruber V, Theisen M;

PI Rance I, Gruber V, Theisen M;

PI Rance I, Gruber V, Theisen M;

PI Rance I, Gruber V, Theisen M;

Query Match 72.6%; Score 285.2; DB 21; Length 472;  
Best Local Similarity 98.1%; Pred. No. 1.2e-77;  
Matches 310; Conservative 0; Mismatches 3; Indels 3; Gaps 2;

```
OY 78 CATGACACTCTGTGCGAATATTGAAAGCGTAAGCACTGACGACACATATGAAAGAAAGA 137
Db 160 CATGACACTCTGTGCGAATATTGAAAGCGTAAGCACTGACGACACATATGAAAGAAAGA 219
OY 138 GATTAAGTCGGTATGTTGTAAGAGACATAGAGACATAGTAAGTGGAAATGTAAG 197
Db 220 GATTAAGTCGGTATGTTGTAAGAGACATAGAGACATAGTAAGTGGAAATGTAAG 278
OY 198 GCGGAAGTAACCTTATGCAATTTGTAATTTGTTAGCACTAGTATGATGATATCAA 257
Db 279 GCGGAAGTAACCTTATGCAATTTGTAATTTGTTAGCACTAGTATGATGATATCAA 338
OY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCAGCTTACCGGATGCC 317
Db 339 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCAGCTTACCGGATGCC 398
OY 318 GGTTCCTCAAGCTTATTTCTTATTAAGCACTGTGTAGTGTAGTAAAGAAACCAACACA 377
Db 399 GGTTCCTCAAGCTTATTTCTTATTAAGCACTGTGTAGTGTAGTAAAGAAACCAACACA 456
OY 378 ACAACCTAGAGATCC 393
Db 457 ACAACCTAGAGATCC 472
```

RESULT 6  
AAA96837

ID AAA96837 standard; DNA; 317 BP.

AC AAA96837;

DT 19-FEB-2001 (first entry)

DE Nucleotide sequence of chimeric expression promoter MP1116.

KW Promoter; intergenic region; Commelina yellow mottle virus;

KW chimeric expression promoter; plant vascular expression promoter;

KW plant green tissue expression promoter; Cassava vein mosaic virus;

KW transgenic plant; chimera; ss.

OS Chimeric - Commelina yellow mottle virus.

OS Chimeric - Cassava vein mosaic virus.

PN WO200058485-A1.

PD 05-OCT-2000.

PF 29-MAR-2000; 2000MO-IB00370.

PR 29-MAR-1999; 99FR-0003925.

PA (MERI-) MERISTEM THERAPEUTICS.

PI Rance I, Gruber V, Theisen M;

PI Rance I, Gruber V, Theisen M;

PI Rance I, Gruber V, Theisen M;

PI Rance I, Gruber V, Theisen M;

PI Rance I, Gruber V, Theisen M;

PI Rance I, Gruber V, Theisen M;

PI Rance I, Gruber V, Theisen M;

PI Rance I, Gruber V, Theisen M;

PI Rance I, Gruber V, Theisen M;





|   |   |  |
|---|---|--|
| PA  | (MERIT-)MERISTEM THERAPEUTICS.  |  |
| XX  |   |  |
| PI  | Rance I, Gruber V, Theisen M;   |  |
| XX  |   |  |
| DR  | WPI: 2000-647238/62.  |  |
| XX  |   |  |
| PT  | Chimeric expression promoter for transgenic plant production, comprises |  |
| PT  | sequence from promoter comprising vascular expression region replaced   |  |
| PT  | with sequence from promoter comprising green tissue expression region   |  |
| XX  |   |  |
| PS  | Claim 5; page 81; 91pp; English.  |  |
| XX  |   |  |
| CC  | The present sequence represents a chimeric promoter of the invention.   |  |
| CC  | The specification describes chimeric expression promoters. These        |  |
| CC  | chimeric promoters comprise a nucleic acid sequence which is derived    |  |
| CC  | from a first plant promoter, in which a plant vascular expression       |  |
| CC  | promoter region is replaced with a nucleic acid sequence derived from   |  |
| CC  | a second plant promoter comprising a plant green tissue expression      |  |
| CC  | promoter region. Preferably, the first plant promoter originates from   |  |
| CC  | Commelina yellow mottle virus, and the second plant promoter originates |  |
| CC  | from the Cassava vein mosaic virus. Especially, the promoters are       |  |
| CC  | derived from intergenic regions. The chimeric promoters are useful      |  |
| CC  | for producing transgenic plants.  |  |
| XX  |   |  |
| SQ  | Sequence 348 BP; 116 A; 70 C; 78 G; 84 T; 0 other;                      |  |
|   | Query Match 51.0%; Score 200.4; DB 21; Length 348;                      |  |
|   | Best Local Similarity 99.1%; Pred. No.1.2e-51;                          |  |
|   | Matches 212; Conservative 0; Mismatches 1; Indels 1; Gaps 1;            |  |
| OY  | 20 ACTAGTATCCGCCGCTCATCATGACATCATCAGCTACTGAGAGATGATAGTACCA 79           |  |
|   |   |  |
| Db  | 52 ACTAGTATCCGCCGCTCATCATGACATCATCAGCTACTGAGAGATGATAGTACCA 111          |  |
| OY  | 80 TGACACTCTGTCGCGAATTTGGAAGACGTAGACATGACAGCAACAATGAAAAGAAAGA 139       |  |
|   |   |  |
| Db  | 112 TGACACTCTGTCGCGAATTTGGAAGACGTAGACATGACAGCAACAATGAAAAGAAAGA 171      |  |
| OY  | 140 TAGAGTCGGTGTGTTGTGAAGAAGACATGAGACACATGTAGGTGAAAATGTAGAGGC 199       |  |
|   |   |  |
| Db  | 172 TAGAGTCGGTGTGTTGTG-AAGAGACATGAGAGACACATGTAGGTGAAAATGTAGAGGC 230     |  |
| OY  | 200 GGAAGTAAACCTTATGACATTGTGTTGGTTAC 233                                |  |
|   |   |  |
| Db  | 231 GGAAGTAAACCTTATGACATTGTGTTGGTTAC 264                                |  |
|   |   |  |
| RESULT 9  |   |  |
| AAA96857  |   |  |
| ID  | AAA96857 standard; DNA: 604 BP.   |  |
| XX  |   |  |
| AC  | AAA96857;   |  |
| XX  |   |  |
| XX  | 19-FEB-2001 (first entry)   |  |
| DE  |   |  |
| XX  |   |  |
| Nucleotide sequence of chimeric expression promoter MP1167. |   |  |
| KW  | Promoter; intergenic region; Commelina yellow mottle virus;             |  |
| KW  | chimeric expression promoter; plant vascular expression promoter;       |  |
| KW  | plant green tissue expression promoter; Cassava vein mosaic virus;      |  |
| KW  | transgenic plant; chimera; ss.  |  |
| XX  |   |  |
| OS  | Chimeric - Commelina yellow mottle virus.                               |  |
| OS  | Chimeric - Cassava vein mosaic virus.                                   |  |
| XX  |   |  |
| PN  | MO200058485-A1.   |  |
| PD  | 05-OCT-2000.  |  |
| XX  |   |  |
| PF  | 29-MAR-2000; 2000MO-IB00370.  |  |
| XX  |   |  |
| PR  | 29-MAR-1999; 99FR-0003925.  |  |

|    |   |   |
|----|---|---|
| XX | (MER1-)   | MERISTEM THERAPEUTICS.  |
| PA | Rance I,  | Gruber V, Theisen M;  |
| PI | WPI;  | 2000-647238/62.   |
| DR |   |   |
| XX |   |   |
| PT | Chimeric expression promoter for transgenic plant production, comprises |   |
| PT | sequence from promoter comprising vascular expression region replaced   |   |
| PT | with sequence from promoter comprising green tissue expression region   |   |
| PS |   |   |
| PS | Claim 5; Page 87; 91pp; English.  |   |
| XX |   |   |
| CC | The present sequence represents a chimeric promoter of the invention.   |   |
| CC | The specification describes chimeric expression promoters. These        |   |
| CC | chimeric promoters comprise a nucleic acid sequence which is derived    |   |
| CC | from a first plant promoter, in which a plant vascular expression       |   |
| CC | promoter region is replaced with a nucleic acid sequence derived from   |   |
| CC | a second plant promoter comprising a plant green tissue expression      |   |
| CC | promoter region. Preferably, the first plant promoter originates from   |   |
| CC | Commelina yellow mottle virus, and the second plant promoter originates |   |
| CC | from the Cassava vein mosaic virus. Especially, the promoters are       |   |
| CC | derived from intergenic regions. The chimeric promoters are useful      |   |
| CC | for producing transgenic plants.  |   |
| SQ | Sequence 604 BP; 186 A; 116 C; 145 G; 157 T; 0 other;                   |   |
|    | Query Match   | 49.9%; Score 196.2; DB 21; Length 604;                            |
|    | Best Local Similarity   | 97.4%; Pred. No. 3e-50;   |
|    | Matches 221; Conservative   | 0; Mismatches 3; Indels 3; Gaps 2.                                |
| QY | 78  | CATGACACTCTGTGGCAATATTGAAGACGTAAAGCAGCTGACGACAACATGAAGAAGAA 137   |
| DB | 160   | CATGCGACACTCTGTGGCAATATTGAAGACGTAAAGCAGCTGACGACAACATGAAGAAGAA 219 |
| QY | 138   | GATAAGGTCGCGTGATTTGGAAAGACATAGAGGACACATGTGAAGTGGAAATGTAAAG 197    |
| DB | 220   | GATAAGGTCGCGTGATTTGGT-AAGAAACATAGAGGACACATGTGAAGTGGAAATGTAAAG 278 |
| QY | 198   | GCGGAACATTAACCTTATGCAATTTGTAATTTGGTTACGACTAGTGAATGTGATATCA 257    |
| DB | 279   | GCGGAACATTAACCTTATGCAATTTGTAATTTGGTTAC--CTACTGATTTGATGATATCA 336  |
| QY | 258   | GATTGATGTGATATCTCCACTGACGCTAAAGGATGACGATGCCACGT 304               |
| DB | 337   | GATTGATGTGATATCTCCACTGACGCTAAAGGATGACGATGCCACGT 383               |
|    | RESULT 10   |   |
|    | AAA96839  |   |
| ID | AAA96839  | standard; DNA; 371 BP.  |
| XX | AAA96839;   |   |
| AC |   |   |
| XX | 19-FEB-2001   | (first entry)   |
| DE |   |   |
| XX | Nucleotide sequence of chimeric expression promoter MPR1146.            |   |
| XX | Promoter; intergenic region; Commelina yellow mottle virus;             |   |
| KW | chimeric expression promoter; plant vascular expression promoter;       |   |
| KW | plant green tissue expression promoter; Cassava vein mosaic virus;      |   |
| KW | transgenic plant; chimera; ss.  |   |
| OS | Chimeric - Commelina yellow mottle virus.                               |   |
| OS | Chimeric - Cassava vein mosaic virus.                                   |   |
| XX | MO200058485-A1.   |   |
| PN |   |   |
| XX | 05-OCT-2000.  |   |
| PD |   |   |
| XX | 29-MAR-2000; 2000WO-IB00370.  |   |
| XX |   |   |

PR 29-MAR-1999; 99FR-0003925.  
XX  
XX (MERI-) MERISTEM THERAPEUTICS.  
XX  
XX Rance I, Gruber V, Theisen M;  
XX  
XX WPI; 2000-647238/52.  
XX  
PT Chimeric expression promoter for transgenic plant production, comprises  
PT sequence from promoter comprising vascular expression region replaced  
PT with sequence from promoter comprising green tissue expression region  
PT  
XX  
XX  
PS Claim 5; Page 81; 91pp; English.  
XX  
XX The present sequence represents a chimeric promoter of the invention.  
CC The specification describes chimeric expression promoters. These  
CC chimeric promoters comprise a nucleic acid sequence which is derived  
CC from a first plant promoter, in which a plant vascular expression  
CC promoter region is replaced with a nucleic acid sequence derived from  
CC a second plant promoter comprising a plant green tissue expression  
CC promoter region. Preferably, the first plant promoter originates from  
CC Commelina yellow mottle virus, and the second plant promoter originates  
CC from the Cassava vein mosaic virus. Especially, the promoters are  
CC derived from intergenic regions. The chimeric promoters are useful  
CC for producing transgenic plants.  
XX  
SQ Sequence 371 BP; 122 A; 68 C; 89 G; 92 T; 0 other;  
XX  
Query Match 39.4%; Score 154.8; DB 21; Length 371;  
Best local Similarity 75.9%; Pred. No. 1.3e-37;  
Matches 240; Conservative 0; Mismatches 2; Indels 74; Gaps 1;  
XX  
OY 78 CATGACACTCTGCGCAATATTGAAGACGTAACTGACGACACAATGAAAGAA 137  
DB 130 CATGCCACTCTGCGCAATATTGAAGACGTAACTGACGACACAATGAAAGAA 189  
OY 138 GATAGGTCGCGTATTGTGAAGACATAGAGACATGTAAAGTGAAGTAAAG 197  
DB 190 GATAGGTCGCGTATTGTGAAGACATAGAGACATGTAAAGTGAAGTAAAG 249  
OY 198 GCGGAAAGTAACCTTATGCACTTTGTAAATGGTTACGACTGATGATCA 257  
DB 250 GCGGAAAGTAACCTTATGCACTTTGTAACTG----- 280  
OY 258 GATTGATGATATCTCCACTGACGTAAAGGATGACGATCCAGCTTACCGGTATGCC 317  
DB 281 -----GTTACCGGTATGCC 295  
OY 318 GGTCCCAAGCTTATTTCTTATTTAAGCACTTGTACTAGCTTAAGAAACCAACACA 377  
DB 296 GGTTCCTCAAGCTTATTTCTTATTTAAGCACTTGTACTAGCTTAAGAAACCAACACA 355  
OY 378 ACAACCTAGAGATCC 393  
DB 356 ACAACCTAGAGATCC 371

RESULT 11  
AAA96841  
ID AAA96841 standard; DNA; 301 BP.  
XX  
XX AAA96841;  
XX  
XX 19-FEB-2001 (first entry)  
XX  
XX Nucleotide sequence of chimeric expression promoter MP1154.  
XX  
XX Promoter; intergenic region; Commelina yellow mottle virus;  
KM chimeric expression promoter; plant vascular expression promoter;  
KM plant green tissue expression promoter; Cassava vein mosaic virus;  
KM transgenic plant; chimera; ss.  
XX

OS Chimeric - Commelina yellow mottle virus.  
OS Chimeric - Cassava vein mosaic virus.  
XX  
XX WO200058485-A1.  
XX  
XX 05-OCT-2000.  
XX  
XX 29-MAR-2000; 2000MO-IB00370.  
XX  
XX 29-MAR-1999; 99FR-0003925.  
XX  
XX (MERI-) MERISTEM THERAPEUTICS.  
XX  
XX Rance I, Gruber V, Theisen M;  
XX  
XX WPI; 2000-647238/52.  
XX  
XX Chimeric expression promoter for transgenic plant production, comprises  
PT sequence from promoter comprising vascular expression region replaced  
PT with sequence from promoter comprising green tissue expression region  
PT  
XX  
XX  
PS Claim 5; Page 82; 91pp; English.  
XX  
XX The present sequence represents a chimeric promoter of the invention.  
CC The specification describes chimeric expression promoters. These  
CC chimeric promoters comprise a nucleic acid sequence which is derived  
CC from a first plant promoter, in which a plant vascular expression  
CC promoter region is replaced with a nucleic acid sequence derived from  
CC a second plant promoter comprising a plant green tissue expression  
CC promoter region. Preferably, the first plant promoter originates from  
CC Commelina yellow mottle virus, and the second plant promoter originates  
CC from the Cassava vein mosaic virus. Especially, the promoters are  
CC derived from intergenic regions. The chimeric promoters are useful  
CC for producing transgenic plants.  
XX  
SQ Sequence 301 BP; 98 A; 54 C; 74 G; 75 T; 0 other;  
XX  
Query Match 35.8%; Score 140.8; DB 21; Length 301;  
Best local Similarity 98.1%; Pred. No. 2.5e-33;  
Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
XX  
OY 78 CATGACACTCTGCGCAATATTGAAGACGTAACTGACGACACAATGAAAGAA 137  
DB 63 CATGCCACTCTGCGCAATATTGAAGACGTAACTGACGACACAATGAAAGAA 122  
OY 138 GATAGGTCGCGTATTGTGAAGACATAGAGACATGTAAAGTGAAGTAAAG 197  
DB 123 GATAGGTCGCGTATTGTG- AAGACATAGAGACATGTAAAGTGAAGTAAAG 181  
OY 198 GCGGAAAGTAACCTTATGCACTTTGTAAATGGTTAC 233  
DB 182 GCGGAAAGTAACCTTATGCACTTTGTAACTGTTAC 217

RESULT 12  
AAA96840  
ID AAA96840 standard; DNA; 398 BP.  
XX  
XX AAA96840;  
XX  
XX 19-FEB-2001 (first entry)  
XX  
XX Nucleotide sequence of chimeric expression promoter MP1147.  
XX  
XX Promoter; intergenic region; Commelina yellow mottle virus;  
KM chimeric expression promoter; plant vascular expression promoter;  
KM plant green tissue expression promoter; Cassava vein mosaic virus;  
KM transgenic plant; chimera; ss.  
XX  
XX Chimeric - Commelina yellow mottle virus.  
OS Chimeric - Cassava vein mosaic virus.  
OS

PN WO20058485-A1.  
XX  
XX 05-OCT-2000.  
PD  
XX 29-MAR-2000; 2000WO-1B00370.  
PF  
XX 29-MAR-1999; 99FR-0003925.  
PR  
XX (MERI-) MERISTEM THERAPEUTICS.  
PA  
XX Rance I, Gruber V, Theisen M;  
PI  
XX WPI; 2000-647238/62.  
DR  
XX  
XX Chimeric expression promoter for transgenic plant production, comprises  
PT sequence from promoter comprising vascular expression region replaced  
PT with sequence from promoter comprising green tissue expression region  
PT  
XX  
XX Claim 5; Page 82; 91pp; English.  
PS  
XX The present sequence represents a chimeric promoter of the invention,  
CC The specification describes chimeric expression promoters. These  
CC chimeric promoters comprise a nucleic acid sequence which is derived  
CC from a first plant promoter, in which a plant vascular expression  
CC promoter region is replaced with a nucleic acid sequence derived from  
CC a second plant promoter comprising a plant green tissue expression  
CC promoter region. Preferably, the first plant promoter originates from  
CC Comellina yellow mottle virus, and the second plant promoter originates  
CC from the cassava vein mosaic virus. Especially, the promoters are  
CC derived from intergenic regions. The chimeric promoters are useful  
CC for producing transgenic plants.  
CC  
SQ Sequence 398 BP; 128 A; 80 C; 93 G; 97 T; 0 other;  
XX  
XX  
XX Query Match 35.8%; Score 140.8; DB 21; Length 398;  
Best Local Similarity 98.1%; Pred. No. 2.8e-33;  
Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
OY 78 CATGACACTCTGTGCGAATATTGAAAGCGTAAGCACTGACGACACATGAAAGAAGAA 137  
DB 160 CATGCCACTCTGTGCGAATATTGAAAGCGTAAGCACTGACGACACATGAAAGAAGAA 219  
OY 138 GATAAGGTGCGGATTTGTGAAGAGACATAGAGACACATGTAAAGTGAAGAAATGTAAG 197  
DB 220 GATAAGGTGCGGATTTGTG- AAGAGACATAGAGACACATGTAAAGTGAAGAAATGTAAG 278  
OY 198 GCGGAAGTAACCTTATGATTTGTAATTGCTTAC 233  
DB 279 GCGGAAGTAACCTTATGATTTGTAATTGCTTAC 314  
RESULT 13  
AAV14019  
ID AAV14019 standard; DNA; 392 BP.  
XX  
XX AAV14019;  
AC  
XX  
XX 18-JUN-1998 (first entry)  
DT  
XX  
XX CSVWV promoter CVPL.  
DE  
XX  
XX Cassava vein mosaic virus; CSVWV; promoter; cultivated crop;  
KW tissue-specific expression control; transgenic plant; ss.  
XX  
XX Cassava vein mosaic virus.  
OS  
XX  
XX WO9748819-A1.  
PN  
XX  
XX 24-DEC-1997.  
PD  
XX  
XX 20-JUN-1997; 97WO-US10376.  
PF  
XX

PR 20-JUN-1996; 96US-0020129.  
XX  
XX (SCRI) SCRIPPS RES INST.  
PA  
XX  
XX Beachy RN, De Kochko A, Fauquet C, Verdaguer B;  
PI  
XX  
XX WPI; 1998-063157/06.  
DR  
XX  
XX Cassava vein mosaic virus promoter - used to express heterologous  
PT DNA sequences for producing transgenic plants having altered  
PT phenotype(s)  
PT  
XX  
XX Claim 2; Page 74; 115pp; English.  
PS  
XX  
XX This sequence represents a cassava vein mosaic virus promoter, and  
CC is a nucleic acid molecule of the invention. The promoter is capable of  
CC initiating transcription of an operably linked heterologous nucleic acid  
CC sequence in a plant cell. The CSVWV promoters are active in both monocot  
CC and dicot plant species, and therefore can be readily applied to a  
CC variety of cultivated crops. Although generally constitutive, the  
CC derivative promoters include promoters that can regulate expression in a  
CC tissue-specific manner, and therefore are useful for controlling  
CC expression of heterologous genes in a tissue-specific manner. The  
CC promoters can be used for producing transgenic plants with an altered  
CC phenotype.  
CC  
SQ Sequence 392 BP; 154 A; 64 C; 83 G; 91 T; 0 other;  
XX  
XX  
XX Query Match 30.7%; Score 120.6; DB 19; Length 392;  
Best Local Similarity 93.3%; Pred. No. 4.5e-27;  
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
OY 93 GAATATTGAAGACGTAAAGCACTGACGACACAAATGAAAGAAAGATTAAGTCGCTGAT 152  
DB 143 GAATCTTGAAGACGTAAAGCACTGACGACACAAATGAAAGAAAGATTAAGTCGCTGAT 202  
OY 153 TGTGAAGAGACATTAAGGACACATGTAAGTGAAGAAATGTAAGCGCGAAATTAACCTT 212  
DB 203 TGTGAAGAGACATTAAGGACACATGTAAGTGAAGAAATGTAAGCGCGAAATTAACCTT 262  
OY 213 ATGCATTGTGAATTT 227  
DB 263 ATGCACAAAGCAATCT 277  
RESULT 14  
AAV14021  
ID AAV14021 standard; DNA; 411 BP.  
XX  
XX AAV14021;  
AC  
XX  
XX 18-JUN-1998 (first entry)  
DT  
XX  
XX CSVWV promoter PB.  
DE  
XX  
XX Cassava vein mosaic virus; CSVWV; promoter; cultivated crop;  
KW tissue-specific expression control; transgenic plant; ss.  
XX  
XX Cassava vein mosaic virus.  
OS  
XX  
XX WO9748819-A1.  
PN  
XX  
XX 24-DEC-1997.  
PD  
XX  
XX 20-JUN-1997; 97WO-US10376.  
PF  
XX  
XX 20-JUN-1996; 96US-0020129.  
PR  
XX  
XX (SCRI) SCRIPPS RES INST.  
PA  
XX  
XX Beachy RN, De Kochko A, Fauquet C, Verdaguer B;  
PI  
XX  
XX WPI; 1998-063157/06.  
DR

XX Cassava vein mosaic virus promoter - used to express heterologous  
PT DNA sequences for producing transgenic plants having altered  
PT phenotype(s)  
XX  
PS Claim 2; Page 76-77; 115pp; English.  
XX  
CC This sequence represents a cassava vein mosaic virus promoter, and  
CC is a nucleic acid molecule of the invention. The promoter is capable of  
CC initiating transcription of an operably linked heterologous nucleic acid  
CC sequence in a plant cell. The CSVMV promoters are active in both monocot  
CC and dicot plant species, and therefore can be readily applied to a  
CC variety of cultivated crops. Although generally constitutive, the  
CC derivative promoters include promoters that can regulate expression in a  
CC tissue-specific manner, and therefore are useful for controlling  
CC expression of heterologous genes in a tissue-specific manner. The  
CC promoters can be used for producing transgenic plants with an altered  
CC phenotype.  
XX  
XX Sequence 411 BP; 157 A; 60 C; 87 G; 107 T; 0 other;  
SO  
Query Match 30.7%; Score 120.6; DB 19; Length 411;  
Best Local Similarity 93.3%; Pred. No. 4.5e-27;  
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
OY 93 GAATTTGAAGACGTAAGCACTGACGACACATGAAAGAAAGATAGTGGTGAT 152  
DB 107 GAATCTTGAAGACGTAAGCACTGACGACACATGAAAGAAAGATAGTGGTGAT 166  
OY 153 TGTGAAGAAGACATAGAGACACATGTAAAGTGAAGGCGGAAAGTAACCTT 212  
DB 167 TGTGAAGAAGACATAGAGACACATGTAAAGTGAAGGCGGAAAGTAACCTT 226  
OY 213 ATGCATTTGTAATTT 227  
DB 227 ATCACAAAGAAATCT 241  
RESULT 15  
AAA96836  
ID AAA96836 standard; DNA; 515 BP.  
XX  
AC AAA96836;  
XX  
DT 19-FEB-2001 (first entry)  
XX  
DE Promoter from intergenic region of Cassava vein mosaic virus.  
XX  
KW Promoter; intergenic region; Commelina yellow mottle virus;  
KW chimeric expression promoter; plant vascular expression promoter;  
KW plant green tissue expression promoter; Cassava vein mosaic virus;  
KW transgenic plant; ss.  
XX  
OS Cassava vein mosaic virus.  
XX  
PN WO200058485-A1.  
XX  
PD 05-OCT-2000.  
XX  
PF 29-MAR-2000; 2000WO-IB00370.  
XX  
PR 29-MAR-1999; 99FR-0003925.  
XX  
PA (MERIT-) MERISTEM THERAPEUTICS.  
XX  
PI Rance I, Gruber V, Theisen M;  
XX  
DR WPI; 2000-647238/62.  
XX  
PT Chimeric expression promoter for transgenic plant production, comprises  
PT sequence from promoter comprising vascular expression region replaced  
PT with sequence from promoter comprising green tissue expression region  
PT

XX  
PS Claim 4; Page 80; 91pp; English.  
XX  
CC The present sequence represents a promoter fragment from the intergenic  
CC region of Cassava vein mosaic virus. The promoter is used to construct  
CC chimeric expression promoters. These chimeric promoters comprise a  
CC nucleic acid sequence which is derived from a first plant promoter,  
CC in which a plant vascular expression promoter region is replaced with  
CC a nucleic acid sequence derived from a second plant promoter comprising  
CC a plant green tissue expression promoter region. Preferably, the first  
CC plant promoter originates from Commelina yellow mottle virus, and the  
CC second plant promoter originates from the Cassava vein mosaic virus.  
CC The chimeric promoters are useful for producing transgenic plants.  
XX  
XX Sequence 515 BP; 198 A; 79 C; 109 G; 129 T; 0 other;  
SO  
Query Match 30.7%; Score 120.6; DB 21; Length 515;  
Best Local Similarity 93.3%; Pred. No. 5e-27;  
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
OY 93 GAATTTGAAGACGTAAGCACTGACGACACATGAAAGAAAGATAGTGGTGAT 152  
DB 216 GAATCTTGAAGACGTAAGCACTGACGACACATGAAAGAAAGATAGTGGTGAT 275  
OY 153 TGTGAAGAAGACATAGAGACACATGTAAAGTGAAGGCGGAAAGTAACCTT 212  
DB 276 TGTGAAGAAGACATAGAGACACATGTAAAGTGAAGGCGGAAAGTAACCTT 335  
OY 213 ATGCATTTGTAATTT 227  
DB 336 ATCACAAAGAAATCT 350

Search completed: April 14, 2003, 08:19:36  
Job time : 129.948 secs



GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 08:01:47 ; Search time 40.5155 Seconds  
(without alignments)  
2974.765 Million cell updates/sec

Title: US-09-963-803-19

Perfect score: 393  
Sequence: 1 aagctgcacgcctgcagca.....cacacaactagagatcc 393

Scoring table: IDENTITY-NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Issued\_Patents\_NA: \*  
1: /cgn2\_6/p1odata/1/ina/5A.COMB.seq: \*  
2: /cgn2\_6/p1odata/1/ina/5B.COMB.seq: \*  
3: /cgn2\_6/p1odata/1/ina/6A.COMB.seq: \*  
4: /cgn2\_6/p1odata/1/ina/6B.COMB.seq: \*  
5: /cgn2\_6/p1odata/1/ina/PCrUS.COMB.seq: \*  
6: /cgn2\_6/p1odata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID                  | Description        |
|------------|-------|-------------|--------|---------------------|--------------------|
| 1          | 44.4  | 11.3        | 7218   | 1 US-08-232-463-14  | Sequence 14, Appl  |
| 2          | 39    | 9.9         | 439    | 1 US-08-247-809A-3  | Sequence 3, Appl   |
| 3          | 39    | 9.9         | 439    | 2 US-08-711-728-3   | Sequence 3, Appl   |
| 4          | 39    | 9.9         | 446    | 1 US-08-764-100-23  | Sequence 23, Appl  |
| 5          | 39    | 9.9         | 532    | 4 US-09-042-126-1   | Sequence 1, Appl   |
| 6          | 39    | 9.9         | 532    | 4 US-09-291-238-1   | Sequence 1, Appl   |
| 7          | 39    | 9.9         | 532    | 4 US-09-330-760-1   | Sequence 1, Appl   |
| 8          | 39    | 9.9         | 532    | 4 US-09-328-473-1   | Sequence 1, Appl   |
| 9          | 39    | 9.9         | 532    | 4 US-09-330-737-1   | Sequence 1, Appl   |
| 10         | 39    | 9.9         | 532    | 4 US-09-329-169-1   | Sequence 1, Appl   |
| 11         | 39    | 9.9         | 532    | 4 US-09-330-714A-1  | Sequence 1, Appl   |
| 12         | 39    | 9.9         | 532    | 4 US-09-328-826-1   | Sequence 1, Appl   |
| 13         | 39    | 9.9         | 560    | 3 US-09-424-26-5    | Sequence 5, Appl   |
| 14         | 39    | 9.9         | 560    | 4 US-09-291-238-5   | Sequence 5, Appl   |
| 15         | 39    | 9.9         | 560    | 4 US-09-330-760-5   | Sequence 5, Appl   |
| 16         | 39    | 9.9         | 560    | 4 US-09-328-473-5   | Sequence 5, Appl   |
| 17         | 39    | 9.9         | 560    | 4 US-09-330-737-5   | Sequence 5, Appl   |
| 18         | 39    | 9.9         | 560    | 4 US-09-329-169-5   | Sequence 5, Appl   |
| 19         | 39    | 9.9         | 560    | 4 US-09-330-714A-5  | Sequence 5, Appl   |
| 20         | 39    | 9.9         | 661    | 4 US-09-328-826-5   | Sequence 5, Appl   |
| 21         | 39    | 9.9         | 661    | 4 US-09-027-998A-33 | Sequence 33, Appl  |
| 22         | 39    | 9.9         | 793    | 1 US-08-371-764-1   | Sequence 1, Appl   |
| 23         | 39    | 9.9         | 793    | 4 US-08-897-736-1   | Sequence 1, Appl   |
| 24         | 39    | 9.9         | 831    | 1 US-08-450-834-5   | Sequence 5, Appl   |
| 25         | 39    | 9.9         | 950    | 6 5177308-3         | Patent No. 5177308 |
| 26         | 39    | 9.9         | 978    | 1 US-08-446-486-31  | Sequence 31, Appl  |
| 27         | 39    | 9.9         | 978    | 1 US-08-463-308-31  | Sequence 31, Appl  |

|    |    |     |      |                     |                    |
|----|----|-----|------|---------------------|--------------------|
| 28 | 39 | 9.9 | 979  | 1 US-08-446-486-30  | Sequence 30, Appl  |
| 29 | 39 | 9.9 | 979  | 1 US-08-463-308-30  | Sequence 30, Appl  |
| 30 | 39 | 9.9 | 980  | 6 5254799-30        | Patent No. 5254799 |
| 31 | 39 | 9.9 | 1030 | 1 US-07-936-163-46  | Sequence 46, Appl  |
| 32 | 39 | 9.9 | 1030 | 4 US-08-729-601A-43 | Sequence 43, Appl  |
| 33 | 39 | 9.9 | 1034 | 4 US-09-363-970-35  | Sequence 35, Appl  |
| 34 | 39 | 9.9 | 1138 | 4 US-09-011-151-8   | Sequence 8, Appl   |
| 35 | 39 | 9.9 | 1138 | 4 US-09-011-151-9   | Sequence 9, Appl   |
| 36 | 39 | 9.9 | 1196 | 4 US-08-729-601A-46 | Sequence 46, Appl  |
| 37 | 39 | 9.9 | 1279 | 4 US-09-185-244-2   | Sequence 2, Appl   |
| 38 | 39 | 9.9 | 1279 | 4 US-09-471-913-6   | Sequence 6, Appl   |
| 39 | 39 | 9.9 | 1303 | 4 US-08-894-440-2   | Sequence 2, Appl   |
| 40 | 39 | 9.9 | 1303 | 4 US-09-458-093-2   | Sequence 2, Appl   |
| 41 | 39 | 9.9 | 1651 | 3 US-09-065-999-5   | Sequence 5, Appl   |
| 42 | 39 | 9.9 | 1651 | 3 US-09-065-999-6   | Sequence 6, Appl   |
| 43 | 39 | 9.9 | 1722 | 1 US-08-247-809A-5  | Sequence 5, Appl   |
| 44 | 39 | 9.9 | 1722 | 2 US-08-711-728-5   | Sequence 5, Appl   |
| 45 | 39 | 9.9 | 1829 | 1 US-07-966-187-17  | Sequence 17, Appl  |

#### ALIGNMENTS

RESULT 1  
US-08-232-463-14/C  
Sequence 14, Application US/08232463  
Patent No. 5670367.  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEIFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOXLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
CLASSIFICATION: 435  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZgpt-Fls  
US-08-232-463-14  
Query Match 11.3% Score 44.4; DB 1; Length 7218;





APPLICANT: Goldbach, Robert W.  
TITLE OF INVENTION: Improvements in or Relating to Organic  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sandoz Agro, Inc  
STREET: 975 California Avenue  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/764,100  
FILING DATE: 06-DEC-1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/214,064  
FILING DATE:  
APPLICATION NUMBER: US 08/032,235  
FILING DATE: 17-MAR-1993  
APPLICATION NUMBER: GB 9206016.9  
FILING DATE: 19-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 57737001s, Allen E.  
REGISTRATION NUMBER: 34,490  
REFERENCE/DOCKET NUMBER: 137-1061  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 354-3592  
TELEFAX: (415) 857-1125  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 446 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-764-100-23

Query Match 9.9%; Score 39; DB 1; Length 446;  
Best Local Similarity 100.0%; Pred. No. 0.0074;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 258 GATTGATGTATATCTCCACTGACGTAAAGGATGACGCA 296  
|||||  
Db 274 GATTGATGTATATCTCCACTGACGTAAAGGATGACGCA 312

RESULT 5  
US-09-042-426-1  
Sequence 1, Application US/09042426  
Patent No. 6114608  
GENERAL INFORMATION:  
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi  
TITLE OF INVENTION: DNA Construct Containing Bacillus  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6114608artis Corporation  
STREET: 564 Morris Avenue  
CITY: Summit  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07901  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,426

FILING DATE: March 13, 1998  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoxie, Thomas  
REGISTRATION NUMBER: 32,993  
REFERENCE/DOCKET NUMBER: 135/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8614  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 532 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
MOLECULE TYPE: linear  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: 35S Promoter  
US-09-042-426-1

Query Match 9.9%; Score 39; DB 3; Length 532;  
Best Local Similarity 100.0%; Pred. No. 0.0079;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 258 GATTGATGTATATCTCCACTGACGTAAAGGATGACGCA 296  
|||||  
Db 274 GATTGATGTATATCTCCACTGACGTAAAGGATGACGCA 312

RESULT 6  
US-09-291-238-1  
Sequence 1, Application US/09291238  
Patent No. 6222104  
GENERAL INFORMATION:  
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi  
TITLE OF INVENTION: DNA Construct Containing Bacillus  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6222104artis Corporation  
STREET: 564 Morris Avenue  
CITY: Summit  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07901  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/291,238  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/042,426  
FILING DATE: March 13, 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoxie, Thomas  
REGISTRATION NUMBER: 32,993  
REFERENCE/DOCKET NUMBER: 135/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8614  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 532 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
MOLECULE TYPE: linear  
HYPOTHETICAL: NO

ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: 35S Promoter  
US-09-291-238-1

Query Match 9.9%; Score 39; DB 4; Length 532;  
Best Local Similarity 100.0%; Pred. No. 0.0079;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAAGGATGACGCA 296  
DB 274 GATTGATGATATCTCCACTGACGTAAGGATGACGCA 312

## RESULT 7

US-09-330-760-1  
Sequence 1, Application US/09330760  
Patent No. 6229075  
GENERAL INFORMATION:  
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi  
TITLE OF INVENTION: DNA Construct Containing Bacillus  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6229075artis Corporation  
STREET: 564 Morris Avenue  
CITY: Summit  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07901  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/330,760  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/042,426  
FILING DATE: March 13, 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoxie, Thomas  
REGISTRATION NUMBER: 32,993  
REFERENCE/DOCKET NUMBER: 135/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8614  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 532 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: 35S Promoter  
US-09-330-760-1

Query Match 9.9%; Score 39; DB 4; Length 532;  
Best Local Similarity 100.0%; Pred. No. 0.0079;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAAGGATGACGCA 296  
DB 274 GATTGATGATATCTCCACTGACGTAAGGATGACGCA 312

RESULT 8  
US-09-328-473-1  
Sequence 1, Application US/09328473

Patent No. 6232533  
GENERAL INFORMATION:  
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi  
TITLE OF INVENTION: DNA Construct Containing Bacillus  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6232533artis Corporation  
STREET: 564 Morris Avenue  
CITY: Summit  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07901  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/328,473  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/042,426  
FILING DATE: March 13, 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoxie, Thomas  
REGISTRATION NUMBER: 32,993  
REFERENCE/DOCKET NUMBER: 135/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8614  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 532 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: 35S Promoter  
US-09-328-473-1

Query Match 9.9%; Score 39; DB 4; Length 532;  
Best Local Similarity 100.0%; Pred. No. 0.0079;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAAGGATGACGCA 296  
DB 274 GATTGATGATATCTCCACTGACGTAAGGATGACGCA 312

## RESULT 9

US-09-330-737-1  
Sequence 1, Application US/09330737  
Patent No. 6232534  
GENERAL INFORMATION:  
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi  
TITLE OF INVENTION: DNA Construct Containing Bacillus  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6232534artis Corporation  
STREET: 564 Morris Avenue  
CITY: Summit  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07901  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25



OY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 296  
Db 274 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 312

## RESULT 12

US-09-328-826-1  
Sequence 1, Application US/09328826  
Patent No. 6399860

## GENERAL INFORMATION:

APPLICANT: Irvlin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi  
TITLE OF INVENTION: DNA Construct Containing Bacillus  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: No. 6399860artis Corporation  
STREET: 564 Morris Avenue  
CITY: Summit  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07901  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/328,826  
FILING DATE: 09-Jun-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,426  
FILING DATE: March 13, 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoxie, Thomas  
REGISTRATION NUMBER: 32,993  
REFERENCE/DOCKET NUMBER: 135/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8614  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 532 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
MOLECULE TYPE: DNA (genomic)  
TOPOLOGY: linear  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: 35S Promoter  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-328-826-1

Query Match 9.9%; Score 39; DB 4; Length 532;  
Best Local Similarity 100.0%; Pred. No. 0.0079;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 296  
Db 274 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 312

## RESULT 13

US-09-042-426-5  
Sequence 5, Application US/09042426  
Patent No. 6114608

GENERAL INFORMATION:  
APPLICANT: Irvlin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi  
TITLE OF INVENTION: DNA Construct Containing Bacillus  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: No. 6114608artis Corporation  
STREET: 564 Morris Avenue

CITY: Summit  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07901

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,426  
FILING DATE: March 13, 1998  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoxie, Thomas  
REGISTRATION NUMBER: 32,993  
REFERENCE/DOCKET NUMBER: 135/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8614  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: 35S Promoter  
US-09-042-426-5

Query Match 9.9%; Score 39; DB 3; Length 560;  
Best Local Similarity 100.0%; Pred. No. 0.0081;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 296  
Db 322 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 360

## RESULT 14

US-09-291-238-5  
Sequence 5, Application US/09291238  
Patent No. 6222104

GENERAL INFORMATION:  
APPLICANT: Irvlin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi  
TITLE OF INVENTION: DNA Construct Containing Bacillus  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: No. 6222104artis Corporation  
STREET: 564 Morris Avenue  
CITY: Summit  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07901  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/291,238  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/042,426  
FILING DATE: March 13, 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoxie, Thomas  
REGISTRATION NUMBER: 32,993  
REFERENCE/DOCKET NUMBER: 135/1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8614  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: 35S Promoter  
US-09-291-238-5

Query Match 9.9%; Score 39; DB 4; Length 560;  
Best Local Similarity 100.0%; Pred. No. 0.0081;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAAGGATGACGCA 296  
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DB 322 GATTGATGATATCTCCACTGACGTAAGGATGACGCA 360

## RESULT 15

US-09-330-760-5  
Sequence 5, Application US/09330760  
Patent No. 6229075  
GENERAL INFORMATION:  
APPLICANT: Irvln J. Mettler, Paul S. Dietrich, Ralph Sinibaldi  
TITLE OF INVENTION: DNA Construct Containing Bacillus  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 622907sartis Corporation  
STREET: 564 Morris Avenue  
CITY: Summit  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07901  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/330,760  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/042,426  
FILING DATE: March 13, 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoxie, Thomas  
REGISTRATION NUMBER: 32,993  
REFERENCE/DOCKET NUMBER: 135/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8614  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: 35S Promoter  
US-09-330-760-5

Query Match

9.9%; Score 39; DB 4; Length 560;

Best Local Similarity 100.0%; Pred. No. 0.0081;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAAGGATGACGCA 296  
|||||  
DB 322 GATTGATGATATCTCCACTGACGTAAGGATGACGCA 360

Search completed: April 14, 2003, 10:28:30  
Job time : 47.515 secs



GenCore version 5.1.4.p5\_A578  
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:29:46 ; Search time 47.268 Seconds  
(without alignments) 7293.024 Million cell updates/sec

Title: US-09-963-803-19  
Perfect score: 393  
Sequence: 1 aagcttcgcatgcctgcagca.....cacacaacactagagatcc 393

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCR\_NEM\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEM\_PUB.seq:\*  
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6: /cgn2\_6/ptodata/1/pubpna/PCRUS\_PUBCOMB.seq:\*  
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13: /cgn2\_6/ptodata/1/pubpna/US60\_NEM\_PUB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description      |
|------------|-------|-------------|--------|----|------------------|
| 1          | 393   | 100.0       | 393    | 9  | US-09-963-803-19 |
| 2          | 314   | 79.9        | 462    | 9  | US-09-963-803-20 |
| 3          | 310   | 78.9        | 392    | 9  | US-09-963-803-21 |
| 4          | 304.6 | 77.5        | 600    | 9  | US-09-963-803-22 |
| 5          | 285.2 | 72.6        | 472    | 9  | US-09-963-803-25 |
| 6          | 212.4 | 54.6        | 317    | 9  | US-09-963-803-3  |
| 7          | 212.4 | 54.0        | 541    | 9  | US-09-963-803-24 |
| 8          | 200.4 | 51.0        | 348    | 9  | US-09-963-803-4  |
| 9          | 196.2 | 49.9        | 604    | 9  | US-09-963-803-23 |
| 10         | 154.8 | 39.4        | 371    | 9  | US-09-963-803-5  |
| 11         | 140.8 | 35.8        | 301    | 9  | US-09-963-803-7  |
| 12         | 140.8 | 35.8        | 398    | 9  | US-09-963-803-6  |
| 13         | 120.6 | 30.7        | 515    | 9  | US-09-963-803-2  |
| 14         | 120.6 | 30.7        | 532    | 9  | US-09-765-555-1  |
| 15         | 120.6 | 30.7        | 8340   | 10 | US-09-847-057-4  |
| 16         | 120.6 | 30.7        | 8340   | 10 | US-09-874-926-4  |
| 17         | 120.6 | 30.7        | 12241  | 12 | US-10-033-190-5  |
| 18         | 80    | 20.4        | 243    | 9  | US-09-963-803-1  |
| 19         | 77.8  | 19.8        | 392    | 9  | US-09-963-803-21 |

|    |      |      |      |    |                   |                   |
|----|------|------|------|----|-------------------|-------------------|
| 20 | 69.6 | 17.7 | 79   | 9  | US-09-963-803-14  | Sequence 14, Appl |
| 21 | 62   | 15.8 | 62   | 9  | US-09-963-803-10  | Sequence 10, Appl |
| 22 | 60   | 15.3 | 60   | 9  | US-09-963-803-9   | Sequence 9, Appl1 |
| 23 | 60   | 15.3 | 63   | 9  | US-09-963-803-12  | Sequence 12, Appl |
| 24 | 58   | 14.8 | 80   | 10 | US-09-870-375-34  | Sequence 34, Appl |
| 25 | 58   | 14.8 | 236  | 10 | US-09-870-375-35  | Sequence 35, Appl |
| 26 | 58   | 14.8 | 299  | 10 | US-09-870-375-36  | Sequence 36, Appl |
| 27 | 58   | 14.8 | 332  | 10 | US-09-870-375-7   | Sequence 7, Appl1 |
| 28 | 58   | 14.8 | 472  | 10 | US-09-870-375-5   | Sequence 5, Appl1 |
| 29 | 55   | 14.0 | 65   | 9  | US-09-963-803-8   | Sequence 8, Appl1 |
| 30 | 55   | 14.0 | 80   | 10 | US-09-870-375-28  | Sequence 28, Appl |
| 31 | 45   | 11.5 | 63   | 9  | US-09-963-803-13  | Sequence 13, Appl |
| 32 | 39.2 | 10.0 | 63   | 10 | US-09-870-375-33  | Sequence 33, Appl |
| 33 | 39.2 | 10.0 | 219  | 10 | US-09-870-375-8   | Sequence 8, Appl1 |
| 34 | 39.2 | 10.0 | 282  | 10 | US-09-870-375-9   | Sequence 9, Appl1 |
| 35 | 39.2 | 10.0 | 315  | 10 | US-09-870-375-10  | Sequence 10, Appl |
| 36 | 39.2 | 10.0 | 381  | 10 | US-09-870-375-15  | Sequence 15, Appl |
| 37 | 39.2 | 10.0 | 455  | 10 | US-09-870-375-6   | Sequence 6, Appl1 |
| 38 | 39.2 | 10.0 | 505  | 10 | US-09-870-375-11  | Sequence 11, Appl |
| 39 | 39   | 9.9  | 566  | 10 | US-09-951-470-3   | Sequence 3, Appl1 |
| 40 | 39   | 9.9  | 661  | 10 | US-09-943-692-33  | Sequence 33, Appl |
| 41 | 39   | 9.9  | 700  | 9  | US-10-138-221-9   | Sequence 9, Appl1 |
| 42 | 39   | 9.9  | 763  | 9  | US-10-162-214-9   | Sequence 9, Appl1 |
| 43 | 39   | 9.9  | 3983 | 10 | US-09-758-987-1   | Sequence 1, Appl1 |
| 44 | 39   | 9.9  | 4973 | 9  | US-09-990-659A-15 | Sequence 15, Appl |
| 45 | 39   | 9.9  | 5767 | 9  | US-09-810-861B-3  | Sequence 3, Appl1 |

ALIGNMENTS

RESULT 1  
US-09-963-803-19  
; Sequence 19, Application US/09963803  
; Publication No. US20030028922A1  
; GENERAL INFORMATION:  
; APPLICANT: Meristem Therapeutics  
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yell  
; FILE REFERENCE: 184332042  
; CURRENT APPLICATION NUMBER: US/09/963, 803  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: FR 99/03925  
; PRIOR FILING DATE: 1999-03-29  
; PRIOR APPLICATION NUMBER: PCT IB00/00370  
; PRIOR FILING DATE: 2000-10-05  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 393  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: promoter MP1162  
; NAME/KEY: promoter  
; LOCATION: (1)..(393)  
; OTHER INFORMATION:  
US-09-963-803-19  
Query Match 100.0%: Score 393; DB 9; Length 393;  
Best Local Similarity 100.0%: Pred. No. 2.1e-109;  
Matches 393: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 AAGCTTCATCCCTGCACACATAGTATCCCGCTATCAATGACATCATCAGTACTGA 60  
Db 1 AAGCTTCATCCCTGCACACATAGTATCCCGCTATCAATGACATCATCAGTACTGA 60  
OY 61 GGAGTGAATGCTAGCCATGACACTGTGTGGGAATATTGAAGACGTAGACGAC 120  
Db 61 GGAGTGAATGCTAGCCATGACACTGTGTGGGAATATTGAAGACGTAGACGAC 120  
OY 121 AACATGAAGAAGACATATAAGTGTGATTTGGAAGAGACATAGACACATGTA 180

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Db 121 AACAAATGAAAGAAAGAAATAGAGTGTGATGTGAAGAGACATAGAGACACATGTA 180  
QY 181 AGGTGCAAAATGTAAAGGGGGAAGTAACCTTATGATGATTTGTAATTTGGTTAGACTAGT 240  
Db 181 AGGTGCAAAATGTAAAGGGGGAAGTAACCTTATGATGATTTGTAATTTGGTTAGACTAGT 240  
QY 241 GATTGATGTGATTCAGATGATGATGATTCACACTGACGTAAAGGATGACGATGCC 300  
Db 241 GATTGATGTGATTCAGATGATGATGATTCACACTGACGTAAAGGATGACGATGCC 300  
QY 301 ACCTTACCCGGTATGCCGGTTCCCAAGCTTATTCCTTATTTAAGCACTTGTAGTAG 360  
Db 301 ACCTTACCCGGTATGCCGGTTCCCAAGCTTATTCCTTATTTAAGCACTTGTAGTAG 360  
QY 361 CTTAGAAACCAACACACAACTAGAGATCC 393  
Db 361 CTTAGAAACCAACACACAACTAGAGATCC 393

RESULT 2  
US-09-963-803-20

Sequence 20, Application US/09963803  
Publication No. US20030028922A1  
GENERAL INFORMATION:  
APPLICANT: Meristem Therapeutics  
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow  
FILE REFERENCE: 184332042  
CURRENT APPLICATION NUMBER: US/09/963,803  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: FR 99/03925  
PRIOR FILING DATE: 1999-03-29  
PRIOR APPLICATION NUMBER: PCT IB00/00370  
PRIOR FILING DATE: 2000-10-05  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 20  
LENGTH: 462  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: promoter MPr1163  
NAME/KEY: promoter  
LOCATION: (1)..(462)  
OTHER INFORMATION:  
US-09-963-803-20

## Query Match

Best Local Similarity 79.9%; Score 314; DB 9; Length 462;  
Matches 393; Conservative 0; Mismatches 0; Indels 69; Gaps 1;

QY 1 AACCTTGCAATGCTGACGACCTAGTATCCGCCCTCATCATGATCATCATAGTACTGA 60  
Db 1 AACCTTGCAATGCTGACGACCTAGTATCCGCCCTCATCATGATCATCATAGTACTGA 60  
QY 61 GGAGATGAATAGCTAGCATGACACTCTGTGCGAATATTGAAGACGTAAAGCATGACGAC 120  
Db 61 GGAGATGAATAGCTAGCATGACACTCTGTGCGAATATTGAAGACGTAAAGCATGACGAC 120  
QY 121 AACCAATGAAAGAAAGAAATAGAGTGTGATGATTTGTAAGAGACATAGAGACATGTA 180  
Db 121 AACCAATGAAAGAAAGAAATAGAGTGTGATGATTTGTAAGAGACATAGAGACATGTA 180  
QY 181 AGGTGCAAAATGTAAAGGGGGAAGTAACCTTATGATGATTTGTAATTTGGTT 231  
Db 181 AGGTGCAAAATGTAAAGGGGGAAGTAACCTTATGATGATTTGTAATTTGGTTAGACTAGT 240  
QY 232 ----- 231  
Db 241 GATTGATGTGATTCAGATGATGATGATTCACACTGACGTAAAGGATGACGATGCC 300

QY 232 ACAGTAGTGTATGATGTATATCAAGATTGATGATATCTCCACTGACGTAAAGGATG 291  
Db 301 ACAGTAGTGTATGATGTATATCAAGATTGATGATATCTCCACTGACGTAAAGGATG 360  
QY 292 ACCCATGCCACCTTACCCGGTATGCCGGTTCCCAAGCTTATTTCTTATTTAAGCACTT 351  
Db 361 ACCCATGCCACCTTACCCGGTATGCCGGTTCCCAAGCTTATTTCTTATTTAAGCACTT 420  
QY 352 GTGTAGTACCTTGAAGAAACCAACACAAACCTAGAGATCC 393  
Db 421 GTGTAGTACCTTGAAGAAACCAACACAAACCTAGAGATCC 462

RESULT 3  
US-09-963-803-21

Sequence 21, Application US/09963803  
Publication No. US20030028922A1  
GENERAL INFORMATION:  
APPLICANT: Meristem Therapeutics  
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow  
FILE REFERENCE: 184332042  
CURRENT APPLICATION NUMBER: US/09/963,803  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: FR 99/03925  
PRIOR FILING DATE: 1999-03-29  
PRIOR APPLICATION NUMBER: PCT IB00/00370  
PRIOR FILING DATE: 2000-10-05  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 21  
LENGTH: 392  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: promoter MPr1164  
NAME/KEY: promoter  
LOCATION: (1)..(392)  
OTHER INFORMATION:  
US-09-963-803-21

## Query Match

Best Local Similarity 78.9%; Score 310; DB 9; Length 392;  
Matches 337; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 AACCTTGCAATGCTGACGACCTAGTATCCGCCCTCATCATGATCATCATAGTACTGA 60  
Db 1 AACCTTGCAATGCTGACGACCTAGTATCCGCCCTCATCATGATCATCATAGTACTGA 60  
QY 61 GGAGATGAATAGCTAGCATGACACTCTGTGCGAATATTGAAGACGTAAAGCATGACGAC 120  
Db 61 GGAGATGAATAGCTAGCATGACACTCTGTGCGAATATTGAAGACGTAAAGCATGACGAC 120  
QY 121 AACCAATGAAAGAAAGAAATAGAGTGTGATGATTTGTAAGAGACATAGAGACATGTA 180  
Db 121 AACCAATGAAAGAAAGAAATAGAGTGTGATGATTTGTAAGAGACATAGAGACATGTA 180  
QY 181 AGGTGCAAAATGTAAAGGGGGAAGTAACCTTATGATGATTTGTAATTTGGTTAGACTAGT 240  
Db 181 AGGTGCAAAATGTAAAGGGGGAAGTAACCTTATGATGATTTGTAATTTGGTTAGACTAGT 240  
QY 241 GATTGATGTGATTCAGATGATGATGATTCACACTGACGTAAAGGATGACGATGCC 300  
Db 241 GATTGATGTGATTCAGATGATGATGATTCACACTGACGTAAAGGATGACGATGCC 300  
QY 301 ACCTTACCCGGTATGCCGGTTCCCAAGCTTATTTCTTATTTAAGCACTTGTAGTAG 360  
Db 301 ACCTTACCCGGTATGCCGGTTCCCAAGCTTATTTCTTATTTAAGCACTTGTAGTAG 360  
QY 361 CTTAGAAACCAACACACAACTAGAGATCC 382  
Db 361 CTTAGAAACCAACACACAACTAGAGATCC 382



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RESULT 4
US-09-963-803-22
; Sequence 22, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE OF INVENTION: vitus and cassava vein mosaic vitus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPr1165
; NAME/KEY: promoter
; LOCATION: (1)..(600)
; OTHER INFORMATION:
US-09-963-803-22
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Best Local Similarity 94.3%; Pred. No. 1.5e-82;
Matches 316; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
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QY 1 AACCTTGACATGCTGCAGCACTAGTATCCCGTCATCATGATCATCATCATGATGTA 60
Db 1 AACCTTGACATGCTGCAGCACTAGTATCCCGTCATCATGATCATCATCATGATGTA 60
QY 61 GGAGATGATAGTACGATGACACTCTGTGCGAATATTGAGACGTAACGATGACGAC 120
Db 61 GGAGATGATAGTACGATGACACTCTGTGCGAATATTGAGACGTAACGATGACGAC 120
QY 121 AACATGCAAAAGAAAGAAAGATAGGTGCGTATGTGAAAGACATAGAGACATGTA 180
Db 121 AACATGCAAAAGAAAGAAAGATAGGTGCGTATGTGAAAGACATAGAGACATGTA 180
QY 181 AGGTGCAAAATGTAAGGCGGAAAGTAACTTATGCTTATGTTATGTTAGACTAGT 240
Db 181 AGGTGCAAAATGTAAGGCGGAAAGTAACTTATGCTTATGTTATGTTAGACTAGT 240
QY 241 GATTGATGATATCAAGATTTGATGATATCTCCACTGACGTAAGGATGACGATGCC 300
Db 241 GATTGATGATATCAAGATTTGATGATATCTCCACTGACGTAAGGATGACGATGCC 300
QY 301 ACCTTACCCGGTATGCCGGTTCCCAAGCTTTATTT 335
Db 301 ACCTTACCCGGTATGCCGGTTCCCAAGCTTTATTT 335
US-09-963-803-25
; Sequence 25, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE OF INVENTION: vitus and cassava vein mosaic vitus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
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; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPr1169
; NAME/KEY: promoter
; LOCATION: (1)..(472)
; OTHER INFORMATION:
US-09-963-803-25
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Query Match          72.6%; Score 285.2; DB 9; Length 472;
Best Local Similarity 98.1%; Pred. No. 1e-76;
Matches 310; Conservative 0; Mismatches 3; Indels 3; Gaps 2;
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QY 78 CATGACACTCTGTGCCAATTTTGAAGACGTAAGCACTGACGACACATGAAAGAGAA 137
Db 160 CATGCCACTCTGTGCCAATTTTGAAGACGTAAGCACTGACGACACATGAAAGAGAA 219
QY 138 GATAGGTCGGTATGTGTGAAGACATAGAGACATGACATGTAAGTGGAAATGTAAG 197
Db 220 GATAGGTCGGTATGTGTGAAGACATAGAGACATGACATGTAAGTGGAAATGTAAG 278
QY 198 GCGGAAAGTAACTTATGCAATTTGTAATTTGTTAGCACTGATGATGATATCA 257
Db 279 GCGGAAAGTAACTTATGCAATTTGTAATTTGTTAGCACTGATGATGATATCA 338
QY 258 GATTGATGATATCTCCACTGACGTAAGGATGACGATGACGATGACGATGATGCC 317
Db 339 GATTGATGATATCTCCACTGACGTAAGGATGACGATGACGATGATGCC 398
QY 318 GGTTCACCACTTATTTCTTATTTAGCACTTGTGTACTGATGTAAGAACACACA 377
Db 399 GGTTCACCACTTATTTCTTATTTAA--ACTTGTGTACTGATGTAAGAACACACA 456
QY 378 ACAACCTAGAGATCC 393
Db 457 ACAACCTAGAGATCC 472
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RESULT 6
US-09-963-803-3
; Sequence 3, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE OF INVENTION: vitus and cassava vein mosaic vitus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 317
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter MPr1116
; NAME/KEY: promoter
; LOCATION: (1)..(317)
; OTHER INFORMATION:
US-09-963-803-3
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|                       |        |                    |       |             |
|-----------------------|--------|--------------------|-------|-------------|
| Query Match           | 39.48; | Score 154.8;       | DB 9; | Length 371; |
| Best Local Similarity | 75.98; | Pred. NO. 3.1e-37; |       |             |

Db 182 GCGGAAGTAACTTATGCATTGTAACCTTGGTT

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Db 182 GCGGAAGTAACCTTATGCATTGTACTTGGTTAC 217

|                       |                |   |          |            |
|-----------------------|----------------|---|----------|------------|
| Query Match           | 35.8%          | Score 140.8   | DB 9     | Length 398 |
| Best Local Similarity | 98.1%          | Pred. No. 5.5e-33   |          |            |
| Matches 153           | Conservative 0 | Mismatches 2  | Indels 1 | Gaps 1     |
| OY                    | 78             | CATGCACTCTGTGGCAATATTGAAGACGTAAAGCACTACGACAACAATGAAGAAGAA   | 137      |            |
|                       |                |   |          |            |
| Db                    | 160            | CATGCACTCTGTGGCAATATTGAAGACGTAAAGCACTACGACAACAATGAAGAAGAA   | 219      |            |
| OY                    | 138            | GATAAGTCGGTGATTGTGAAAAGAGACATAGAGACACATGTAAGGTGAAAATGTAAAG  | 197      |            |
|                       |                |   |          |            |
| Db                    | 220            | GATAAGTCGGTGATTGTG - AAGAGACATAGAGACACATGTAAGGTGAAAATGTAAAG | 278      |            |
| OY                    | 198            | GCGGAAGTAACCTATGCACTTTGTGAATTTGGTTAC                        | 233      |            |
|                       |                |   |          |            |
| Db                    | 279            | GCGGAAGTAACCTATGCACTTTGTGAATTTGGTTAC                        | 314      |            |

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: OTHER INFORMATION:
US-09-963-803-2

Query Match          30.7%; Score 120.6; DB 9; Length 515;
Best Local Similarity 93.3%; Pred. No. 8.3e-27;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 93 GAATATTGAAACGCGTAACACTGACGACACAAATGAAAGAAAGAAAGATTAAGTCGGTGAT 152
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 216 GAATCTTGAAGACGTAACCACTGACGACACAAATGAAAGAAAGAAAGATTAAGTCGGTGAT 275

QY 153 TGTGAAAGAGACATTAAGAGACACATGTAAGGTGCGAAATGTAAGGCGCGAAAGTAACCTT 212
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 276 TGTGAAAGAGACATTAAGAGACACATGTAAGGTGCGAAATGTAAGGCGCGAAAGTAACCTT 335

QY 213 ATGCATTTGTAATTT 227
    || || || || ||
Db 336 ATCACAAAGAAATCT 350

RESULT 14
US-09-765-555-1
: Sequence 1, Application US/09765555
: Publication No. US20030037355A1
: GENERAL INFORMATION:
: APPLICANT: The Scripps Research Institute
: TITLE OF INVENTION: Methods and compositions to modulate
: FILE OF INVENTION: expression in plants
: FILE REFERENCE: 27801-20014.40
: CURRENT APPLICATION NUMBER: US/09/765,555
: PRIOR FILING DATE: 2002-05-24
: PRIOR APPLICATION NUMBER: US 09/620,897
: PRIOR FILING DATE: 2000-01-21
: PRIOR APPLICATION NUMBER: US 60/177,468
: PRIOR FILING DATE: 2000-01-21
: NUMBER OF SEQ ID NOS: 75
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 532
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Promoter CSMV
US-09-765-555-1

Query Match          30.7%; Score 120.6; DB 9; Length 532;
Best Local Similarity 93.3%; Pred. No. 8.4e-27;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 93 GAATATTGAAAGCGTAACACTGACGACACAAATGAAAGAAAGAAAGATTAAGTCGGTGAT 152
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 231 GAATCTTGAAGACGTAACCACTGACGACACAAATGAAAGAAAGAAAGATTAAGTCGGTGAT 290

QY 153 TGTGAAAGAGACATTAAGAGACACATGTAAGGTGCGAAATGTAAGGCGCGAAAGTAACCTT 212
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 291 TGTGAAAGAGACATTAAGAGACACATGTAAGGTGCGAAATGTAAGGCGCGAAAGTAACCTT 350

QY 213 ATGCATTTGTAATTT 227
    || || || || ||
Db 351 ATCACAAAGAAATCT 365

RESULT 15
US-09-847-057-4/c
: Sequence 4, Application US/09847057
: Patent No. US2002004943A1
: GENERAL INFORMATION:
: APPLICANT: AGRINOMICS, LLC.
: TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A PAGODA PHENOTYPE IN F
: FILE REFERENCE: PAGODA
: CURRENT APPLICATION NUMBER: US/09/847,057
: CURRENT FILING DATE: 2001-05-01
: NUMBER OF SEQ ID NOS: 4

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 8340
; TYPE: DNA
; ORGANISM: Binary vector pAG14002
US-09-847-057-4

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|                           |       |                    |           |              |
|---------------------------|-------|--------------------|-----------|--------------|
| Query Match               | 30.7% | Score 120.6;       | DB 10;    | Length 8340; |
| Best Local Similarity     | 93.3% | Pred. NO. 3.1e-26; |           |              |
| Matches 126; Conservative | 0;    | Mismatches 9;      | Indels 0; | Gaps 0;      |

| QY | 93   | GAATATTTGAAGACCTTAGCAGCTCAGACACACATGAAAAGAAGATTAAGTGGTAT    | 152  |
|----|------|---|------|
|    |      |   |      |
| Db | 7853 | GAATCTTGAAGAGCTAGAGCACTGACCAACAATGAAAAGAAGATTAAGTGGTAT      | 7734 |
|    |      |   |      |
| QY | 153  | TGCGAAGAGACACTATAGAGACACATCTAGGTGGGAAAATGTAGGCGCGAAAGTAACTT | 212  |
|    |      |   |      |
| Db | 7793 | TGTGAAAGACACTATAGAGACACATCTAGGTGGGAAAATGTAGGCGCGAAAGTAACTT  | 7734 |
|    |      |   |      |
| QY | 213  | ATGCATTGTGAATTT   |      |
|    |      |   |      |
| Db | 7733 | ATCACAAGGAATCTT 7719  |      |

Search completed: April 14, 2003, 12:29:05  
Job time : 50.268 secs

2



GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 08:13:29 ; Search time 1585.51 Seconds  
(without alignments)  
6232.082 Million cell updates/sec

Title: US-09-963-803-19

Perfect score: 393  
Sequence: 1 aagcttgatgcctgcagca.....cacacaacctagagatcc 393

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_NA\_Main:\*

1: /cgn2\_6/ptodata/1/pna/US0600.COMB.seq.\*  
2: /cgn2\_6/ptodata/1/pna/US06.COMB.seq.\*  
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22: /cgn2\_6/ptodata/1/pna/US095D.COMB.seq.\*  
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| Result |       |             |           | SUMMARIES |                   |                   |  |
|--------|-------|-------------|-----------|-----------|-------------------|-------------------|--|
| No.    | Score | Query Match | Length DB | ID        | Description       |                   |  |
| 1      | 393   | 100.0       | 393       | 36        | US-09-963-803-19  | Sequence 19, Appl |  |
| 2      | 314   | 79.9        | 462       | 36        | US-09-963-803-20  | Sequence 20, Appl |  |
| 3      | 310   | 78.9        | 392       | 36        | US-09-963-803-21  | Sequence 21, Appl |  |
| 4      | 304.6 | 77.5        | 600       | 36        | US-09-963-803-22  | Sequence 22, Appl |  |
| 5      | 285.2 | 72.6        | 472       | 36        | US-09-963-803-25  | Sequence 25, Appl |  |
| 6      | 214.4 | 54.6        | 317       | 36        | US-09-963-803-3   | Sequence 3, Appl  |  |
| 7      | 212.4 | 54.0        | 541       | 36        | US-09-963-803-24  | Sequence 24, Appl |  |
| 8      | 200.4 | 51.0        | 348       | 36        | US-09-963-803-23  | Sequence 23, Appl |  |
| 9      | 196.2 | 49.9        | 604       | 36        | US-09-963-803-4   | Sequence 4, Appl  |  |
| 10     | 154.8 | 39.4        | 371       | 36        | US-09-963-803-5   | Sequence 5, Appl  |  |
| 11     | 140.8 | 35.8        | 301       | 36        | US-09-963-803-7   | Sequence 7, Appl  |  |
| 12     | 140.8 | 35.8        | 398       | 36        | US-09-963-803-6   | Sequence 6, Appl  |  |
| 13     | 120.6 | 30.7        | 392       | 1         | PCR-US97-10376-1  | Sequence 1, Appl  |  |
| 14     | 120.6 | 30.7        | 392       | 1         | PCR-US97-10376A-1 | Sequence 1, Appl  |  |
| 15     | 120.6 | 30.7        | 392       | 16        | US-09-202-838A-1  | Sequence 1, Appl  |  |
| 16     | 120.6 | 30.7        | 392       | 16        | US-09-202-838A-1  | Sequence 1, Appl  |  |
| 17     | 120.6 | 30.7        | 411       | 1         | PCR-US97-10376-4  | Sequence 4, Appl  |  |
| 18     | 120.6 | 30.7        | 411       | 1         | PCR-US97-10376A-4 | Sequence 4, Appl  |  |
| 19     | 120.6 | 30.7        | 411       | 16        | US-09-202-838A-4  | Sequence 4, Appl  |  |
| 20     | 120.6 | 30.7        | 411       | 16        | US-09-202-838A-4  | Sequence 4, Appl  |  |
| 21     | 120.6 | 30.7        | 515       | 25        | US-09-641-466-1   | Sequence 1, Appl  |  |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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22 120.6 30.7 515 36 US-09-963-803-2 Sequence 2, Appl1
23 120.6 30.7 524 1 PCT-US97-10376-2 Sequence 2, Appl1
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37 120.6 30.7 12241 35 US-09-948-138-4 Sequence 5, Appl1
38 120.6 30.7 12241 38 US-10-033-190-5 Sequence 5, Appl1
39 120.6 30.7 305 1 PCT-US97-10376-5 Sequence 5, Appl1
40 117.4 29.9 305 1 PCT-US97-10376A-5 Sequence 5, Appl1
41 117.4 29.9 305 16 US-09-202-838-5 Sequence 5, Appl1
42 117.4 29.9 305 16 US-09-202-838A-5 Sequence 5, Appl1
43 117.4 29.9 420 1 PCT-US97-10376-9 Sequence 9, Appl1
44 117.4 29.9 420 1 PCT-US97-10376A-9 Sequence 9, Appl1
45 117.4 29.9 420 1 PCT-US97-10376A-9
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## ALIGNMENTS

```
RESULT 1
US-09-963-803-19
: Sequence 19, Application US/09963803
: GENERAL INFORMATION:
: APPLICANT: Meristem Therapeutics
: TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
: TITLE OF INVENTION: virus and cassava vein mosaic virus
: FILE REFERENCE: 184332042
: CURRENT APPLICATION NUMBER: US/09/963, 803
: PRIOR FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: FR 99/03925
: PRIOR FILING DATE: 1999-03-29
: PRIOR APPLICATION NUMBER: PCT IB00/00370
: PRIOR FILING DATE: 2000-10-05
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 19
: LENGTH: 393
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: promoter Mp1162
: NAME/KEY: promoter
: LOCATION: (1)..(393)
: OTHER INFORMATION:
US-09-963-803-19
```

Query Match 100.0%; Score 393; DB 36; Length 393;

Best Local Similarity 100.0%; Pred. No. 2, 6e-103; Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy 1 AAGCTTGATGCGCTGCAGACACTAGTATCGCGCGTCATCAATGACATCATCAGAGTACTGA 60
    |||
Db 1 AAGCTTGATGCGCTGCAGACACTAGTATCGCGCGTCATCAATGACATCATCAGAGTACTGA 60
Oy 61 GGAGATGATAGTACCTGACACTCTGTGCGAATATTGAAGAGCTAGACACTGACGAC 120
    |||
Db 61 GGAGATGATAGTACCTGACACTCTGTGCGAATATTGAAGAGCTAGACACTGACGAC 120
Oy 121 AACATGAAAAAGACAGATAAGTGCAGTATTGGAAGAGACATAGAGGACACATGTA 180
    |||
Db 121 AACATGAAAAAGACAGATAAGTGCAGTATTGGAAGAGACATAGAGGACACATGTA 180
```

```
Oy 181 AGGTGAAAAATGTAAGGCGGAAAGTAACCTTATGATTTGTTAAATTTGTTACGACTAGT 240
    |||
Db 181 AGGTGAAAAATGTAAGGCGGAAAGTAACCTTATGATTTGTTAAATTTGTTACGACTAGT 240
Oy 241 GATTGATGATATATCAAGATTGATGTGATATCTCCACTGACGTAAGGATGACGATGCC 300
    |||
Db 241 GATTGATGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGATGACGATGCC 300
Oy 301 ACGTTACCGGATGCGGTTCCCAAGCTTATTTCTTATTTAAAGCACTGTGTAGTAGT 360
    |||
Db 301 ACGTTACCGGATGCGGTTCCCAAGCTTATTTCTTATTTAAAGCACTGTGTAGTAGT 360
Oy 361 CTTAGAAAACCAACACACACACTAGAGATCC 393
    |||
Db 361 CTTAGAAAACCAACACACACACTAGAGATCC 393
```

```
RESULT 2
US-09-963-803-20
: Sequence 20, Application US/09963803
: GENERAL INFORMATION:
: APPLICANT: Meristem Therapeutics
: TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
: TITLE OF INVENTION: virus and cassava vein mosaic virus
: FILE REFERENCE: 184332042
: CURRENT APPLICATION NUMBER: US/09/963, 803
: PRIOR FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: FR 99/03925
: PRIOR FILING DATE: 1999-03-29
: PRIOR APPLICATION NUMBER: PCT IB00/00370
: PRIOR FILING DATE: 2000-10-05
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 20
: LENGTH: 462
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: promoter Mp1163
: NAME/KEY: promoter
: LOCATION: (1)..(462)
: OTHER INFORMATION:
US-09-963-803-20
```

Query Match 79.9%; Score 314; DB 36; Length 462;

Best Local Similarity 85.1%; Pred. No. 2, 5e-80; Matches 393; Conservative 0; Mismatches 0; Indels 69; Gaps 1;

```
Oy 1 AAGCTTGATGCGCTGCAGACACTAGTATCGCGCGTCATCAATGACATCATCAGACTACTGA 60
    |||
Db 1 AAGCTTGATGCGCTGCAGACACTAGTATCGCGCGTCATCAATGACATCATCAGACTACTGA 60
Oy 61 GGAGATGATAGTACCTGACACTCTGTGCGAATATTGAAGAGCTAGACACTGACGAC 120
    |||
Db 61 GGAGATGATAGTACCTGACACTCTGTGCGAATATTGAAGAGCTAGACACTGACGAC 120
Oy 121 AACATGAAAAAGACAGATAAGTGCAGTATTGGAAGAGACATAGAGGACACATGTA 180
    |||
Db 121 AACATGAAAAAGACAGATAAGTGCAGTATTGGAAGAGACATAGAGGACACATGTA 180
Oy 181 AGGTGAAAAATGTAAGGCGGAAAGTAACCTTATGATTTGTTAAATTTGTTACGACTAGT 240
    |||
Db 181 AGGTGAAAAATGTAAGGCGGAAAGTAACCTTATGATTTGTTAAATTTGTTACGACTAGT 240
Oy 232 ----- 231
    |||
Db 241 GATTGATGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGATGACGATGCC 300
    |||
Oy 232 ACGACTAGATGATGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGATG 291
    |||
Db 301 ACGACTAGATGATGATATCAAGATTGATGTGATATCTCCACTGACGTAAGGATG 360
```





ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: promoter MPr1169  
FEATURE:  
NAME/KEY: promoter  
LOCATION: (1)..(472)  
OTHER INFORMATION:  
US-09-963-803-25

Query Match 72.6%; Score 285.2; DB 36; Length 472;  
Best Local Similarity 98.1%; Pred. No. 5.8e-72;  
Matches 310; Conservative 0; Mismatches 3; Indels 3; Gaps 2;

QY 78 CATGACACTCTGCGCAATATTGAAGACGTAAAGCAGTACGACGACAAACAATGAAGAAGAA 137  
DB 160 CATGCCACTCTGCGCAATATTGAAGACGTAAAGCAGTACGACGACAAACAATGAAGAAGAA 219  
QY 138 GATTAAGCTCGGTATTTGTGAAGAAGACATAGAGACATGTAAGGTGAAAAATGTAAGG 197  
DB 220 GATTAAGCTCGGTATTTGTG-AAGAGACATAGAGACATAGTAAGGTGAAAAATGTAAGG 278  
QY 198 GCGGAAGTAACCTTATGCTTGTGTAATTTGTTAGACTAGTATGATGATATCA 257  
DB 279 GCGGAAGTAACCTTATGCTTGTGTAATTTGTTAGACTAGTATGATGATATCA 338  
QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCGTTACCGGTATGCC 317  
DB 339 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCGTTACCGGTATGCC 398  
QY 318 GGTTCACCACTTTATTTCTTTATTAAGCAGCTGTGTAGTACCTTAAGAAACCAACACA 377  
DB 399 GGTTCACCACTTTATTTCTTTATTAAGCAGCTGTGTAGTACCTTAAGAAACCAACACA 456  
QY 378 ACAACCTAGAGATCC 393  
DB 457 ACAACCTAGAGATCC 472

## RESULT 6

US-09-963-803-3  
Sequence 3, Application US/09963803  
GENERAL INFORMATION:  
APPLICANT: Meristem Therapeutics  
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow  
FILE REFERENCE: 184332042  
CURRENT APPLICATION NUMBER: US/09/963,803  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: FR 99/03925  
PRIOR FILING DATE: 1999-03-29  
PRIOR APPLICATION NUMBER: PCT IB00/00370  
PRIOR FILING DATE: 2000-10-05  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 317  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Promoter MPr1116  
NAME/KEY: promoter  
LOCATION: (1)..(317)  
OTHER INFORMATION:  
US-09-963-803-3

Query Match 54.6%; Score 214.4; DB 36; Length 317;  
Best Local Similarity 79.9%; Pred. No. 1.9e-51;  
Matches 299; Conservative 0; Mismatches 1; Indels 74; Gaps 1;

QY 20 ACTAGATATCCCGCGTATCAATATACATCATCAAGTACTAGAGATGAATTAAGTACCA 79  
DB 18 ACTAGATATCCCGCGTATCAATATACATCATCAAGTACTAGAGATGAATTAAGTACCA 77

QY 80 TGACACTCTGTGCGAATATTGAAGACGTAAAGCAGTACGACGACAAACAATGAAGAAGAA 139  
DB 78 TGACACTCTGTGCGAATATTGAAGACGTAAAGCAGTACGACGACAAACAATGAAGAAGAA 137  
QY 140 TAAGTCGGTGTATTTGTGAAGAAGACATAGAGACATGTAAGGTGAAAAATGTAAGGCC 199  
DB 138 TAAGTCGGTGTATTTGTGAAGAAGACATAGAGACATGTAAGGTGAAAAATGTAAGGCC 197  
QY 200 GGAATTAACCTTATTCATTTTGTAAATTTGTTAGCACTAGTATGATGATATCA 259  
DB 198 GGAATTAACCTTATTCATTTTGTAAATTTGTTAGCACTAGTATGATGATATCA 226  
QY 260 TTGATGTGATATCTCCAGTACGATAGGATGACGATGCCAGTTACCGGATGCCG 319  
DB 227 -----GTTACCGGATGCCG 243  
QY 320 TTCCCAAGCTTTATTTCTTATTTAAGCACTGTGTAGTACCTTAAGAAACCAACACAC 379  
DB 244 TTCCCAAGCTTTATTTCTTATTTAAGCACTGTGTAGTACCTTAAGAAACCAACACAC 303  
QY 380 AACCTAGAGATCC 393  
DB 304 AACCTAGAGATCC 317

## RESULT 7

US-09-963-803-24  
Sequence 24, Application US/09963803  
GENERAL INFORMATION:  
APPLICANT: Meristem Therapeutics  
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow  
FILE REFERENCE: 184332042  
CURRENT APPLICATION NUMBER: US/09/963,803  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: FR 99/03925  
PRIOR FILING DATE: 1999-03-29  
PRIOR APPLICATION NUMBER: PCT IB00/00370  
PRIOR FILING DATE: 2000-10-05  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 24  
LENGTH: 541  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: promoter MPr1168  
NAME/KEY: promoter  
LOCATION: (1)..(541)  
OTHER INFORMATION:  
US-09-963-803-24

Query Match 54.0%; Score 212.4; DB 36; Length 541;  
Best Local Similarity 91.5%; Pred. No. 8.7e-51;  
Matches 236; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 78 CATGACACTCTGCGCAATATTGAAGACGTAAAGCAGTACGACGACAAACAATGAAGAAGAA 137  
DB 160 CATGCCACTCTGCGCAATATTGAAGACGTAAAGCAGTACGACGACAAACAATGAAGAAGAA 219  
QY 138 GATTAAGCTCGGTATTTGTGAAGAAGACATAGAGACATGTAAGGTGAAAAATGTAAGG 197  
DB 220 GATTAAGCTCGGTATTTGTG-AAGAGACATAGAGACATAGTAAGGTGAAAAATGTAAGG 278  
QY 198 GCGGAAGTAACCTTATGCTTGTGTAATTTGTTAGACTAGTATGATGATATCA 257  
DB 279 GCGGAAGTAACCTTATGCTTGTGTAATTTGTTAGACTAGTATGATGATATCA 338  
QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCGTTACCGGTATGCC 317  
DB 339 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCGTTACCGGTATGCC 398



```
DB 250 GCGGAAAGTAACCTTATGCACTTTGTAACCTG----- 280
QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCACGTTACCGGTATGCC 317
DB 281 -----GTTACCGCGGTATGCC 295
QY 318 GGTTCACAGCTTATTTCTTATTTAAGACACTGTGTAGTACTTAGAAGAACCAACACA 377
DB 296 GGTTCACAGCTTATTTCTTATTTAAGACACTGTGTAGTACTTAGAAGAACCAACACA 355
QY 378 ACAACCTAGAGATCC 393
DB 356 ACAACCTAGAGATCC 371

RESULT 11
US-09-963-803-7
; Sequence 7, Application US/09963803
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter Mpr1154
; NAME/KEY: promoter
; LOCATION: (1)..(301)
; OTHER INFORMATION:
US-09-963-803-7

Query Match 35.8%; Score 140.8; DB 36; Length 301;
Best Local Similarity 98.1%; Pred. No. 4.5e-30;
Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 78 CATGACACTCTGTGCGAATATTGAAGACGTAGACACTGACGACACATGAAAGAA 137
DB 63 CATGCACTCTGTGCGAATATTGAAGACGTAGACACTGACGACACATGAAAGAA 122
QY 138 GATAAGTGGTATTGTGAAGAGACATGAGACATGTAAGGTGAAATGTAAAG 197
DB 123 GATAGTGGTATTGTG-AAAGACATGAGACATGTAAGGTGAAATGTAAAG 181
QY 198 GCGGAAAGTAACCTTATGCACTTTGTAATTTGTTAC 233
DB 182 GCGGAAAGTAACCTTATGCACTTTGTAACCTGTTAC 217

RESULT 12
US-09-963-803-6
; Sequence 6, Application US/09963803
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
```

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; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter Mpr1147
; NAME/KEY: promoter
; LOCATION: (1)..(398)
; OTHER INFORMATION:
US-09-963-803-6

Query Match 35.8%; Score 140.8; DB 36; Length 398;
Best Local Similarity 98.1%; Pred. No. 5e-30;
Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 78 CATGACACTCTGTGCGAATATTGAAGACGTAGACACTGACGACACATGAAAGAA 137
DB 160 CATGCACTCTGTGCGAATATTGAAGACGTAGACACTGACGACACATGAAAGAA 219
QY 138 GATAAGTGGTATTGTGAAGAGACATGAGACATGTAAAGTGAATGTAAAG 197
DB 220 GATAGTGGTATTGTG-AAAGACATGAGACATGTAAAGTGAATGTAAAG 278
QY 198 GCGGAAAGTAACCTTATGCACTTTGTAATTTGTTAC 233
DB 279 GCGGAAAGTAACCTTATGCACTTTGTAACCTGTTAC 314

RESULT 13
PCT-US97-10376-1
; Sequence 1, Application PC/TUS9710376
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: CASSAVA VEIN MOSAIC VIRUS PROMOTERS AND
; FILE REFERENCE: US97/10376
; NUMBER OF SEQUENCES: 36
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/10376
; FILING DATE: 20-JUN-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/020,129
; FILING DATE: 20-JUN-1996
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 392 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; HYPOTHETICAL: NO
; PCT-US97-10376-1

Query Match 30.7%; Score 120.6; DB 1; Length 392;
Best Local Similarity 93.3%; Pred. No. 3.7e-24;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 93 GAATATTGAAGACGTAGACACTGACGACACATGAAAGAAAGATAGGTGGTGTAT 152
DB 143 GATCTTGAAGACGTAGACACTGACGACACATGAAAGAAAGATAGGTGGTGTAT 202
QY 153 TGTGAAGACATGAGACACATGTAAAGGTGAAATGTAAAGGCGGAAAGTAACCTT 212
```

Db 203 TGTGAAGAGACATAGAGACACATGTAAGGTGGAATAATGTAAGCGCGGAAGTAACCTT 262

QY 213 ATGCATTTGTAATTT 227

Db 263 ATCACAAAGCAATCT 277

## RESULT 14

PCT-US97-10376A-1  
; Sequence 1, Application PC/TUS9710376A  
; GENERAL INFORMATION:  
; APPLICANT: Verdaguier, Bertrand  
; APPLICANT: de Kochko, Alexandre  
; APPLICANT: Beachy, Roger N.  
; TITLE OF INVENTION: CASSAVA VEIN MOSAIC VIRUS PROMOTERS AND  
; TITLE OF INVENTION: USES THEREOF  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE  
; STREET: 10550 North Torrey Pines Road  
; CITY: La Jolla  
; STATE: California  
; COUNTRY: US  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US97/10376A  
; FILING DATE: 20-JUN-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/020,129  
; FILING DATE: 20-JUN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: 504.1PC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 784-2937  
; TELEFAX: (619) 784-9399  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 392 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; PCT-US97-10376A-1

Query Match 30.7%; Score 120.6; DB 1; Length 392;

Best Local Similarity 93.3%; Pred. No. 3.7e-24;  
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 93 GAATATTGAAGACGTAGACGTGACGACCAACATGAAAGAGAGAAAGTAAGTCGGTGAT 152

Db 143 GAATCTTGAAGACGTAGACGTGACGACCAACATGAAAGAGAGAAAGTAAGTCGGTGAT 202

QY 153 TGTGAAGAGACATAGAGACACATGTAGGTGAAAAATGTAAGCGCGGAAGTAACCTT 212

Db 203 TGTGAAGAGACATAGAGACACATGTAGGTGAAAAATGTAAGCGCGGAAGTAACCTT 262

QY 213 ATGCATTTGTAATTT 227

Db 263 ATCACAAAGCAATCT 277

RESULT 15

US-09-202-838-1

; Sequence 1, Application US/09202838  
; GENERAL INFORMATION:  
; APPLICANT: Verdaguier, Bertrand  
; APPLICANT: de Kochko, Alexandre  
; APPLICANT: Beachy, Roger N.  
; APPLICANT: Fauquet, Claude  
; TITLE OF INVENTION: CASSAVA VEIN MOSAIC VIRUS PROMOTERS AND USES THEREOF  
; FILE REFERENCE: MYC0115  
; CURRENT APPLICATION NUMBER: US/09/202,838  
; CURRENT FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: PCT/US97/10376  
; PRIOR FILING DATE: 1997-06-20  
; PRIOR APPLICATION NUMBER: 60/020,129  
; PRIOR FILING DATE: 1996-06-20  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 392  
; TYPE: DNA  
; ORGANISM: Cassava vein mosaic virus  
; US-09-202-838-1

Query Match 30.7%; Score 120.6; DB 16; Length 392;

Best Local Similarity 93.3%; Pred. No. 3.7e-24;  
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 93 GAATATTGAAGACGTAGACGTGACGACCAACATGAAAGAGAGAAAGTAAGTCGGTGAT 152

Db 143 GAATCTTGAAGACGTAGACGTGACGACCAACATGAAAGAGAGAAAGTAAGTCGGTGAT 202

QY 153 TGTGAAGAGACATAGAGACACATGTAGGTGAAAAATGTAAGCGCGGAAGTAACCTT 212

Db 203 TGTGAAGAGACATAGAGACACATGTAGGTGAAAAATGTAAGCGCGGAAGTAACCTT 262

QY 213 ATGCATTTGTAATTT 227

Db 263 ATCACAAAGCAATCT 277

Search completed: April 14, 2003, 12:06:29  
Job time : 1588.51 secs





```

RESULT 2
US-09-673-274B-19
: Sequence 19, Application US/09673274B
: GENERAL INFORMATION:
:   APPLICANT: Lamberty, Mireille
:   APPLICANT: Bulet, Phillipe
:   APPLICANT: Brookhart, Gary
:   APPLICANT: Hoffman, Jules
:   TITLE OF INVENTION: GENE CODING FOR HELIOMICINE, AND USE THEREOF
:   FILE REFERENCE: A33595-PCT-USA (0726667.0166)
:   CURRENT APPLICATION NUMBER: US/09/673.274B
:   PRIOR FILING DATE: 1999-04-12
:   PRIOR APPLICATION NUMBER: PCT/FR99/00843
:   PRIOR FILING DATE: 1999-04-12
:   PRIOR APPLICATION NUMBER: FR 98 04933
:   NUMBER OF SEQ ID NOS: 48
:   SOFTWARE: FastSeq for Windows Version 4.0
:   SEQ ID NO 19
:   LENGTH: 838
:   TYPE: DNA
:   ORGANISM: Artificial Sequence
:   FEATURE:
:   OTHER INFORMATION: Synthetic oligonucleotide
:   FEATURE:
:   NAME/KEY: promoter
:   LOCATION: (7)...(532)
:   FEATURE:
:   NAME/KEY: misc_structure
:   LOCATION: (533)...(568)
:   FEATURE:
:   NAME/KEY: terminator
:   LOCATION: (569)...(832)
:   US-09-673-274B-19

Query Match          30.7%; Score 120.6; DB 6; Length 838;
Best Local Similarity 93.3%; Pred. No. 1.4e-25;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      93 GAATATTGAAGACGTAACCTAGCAGCAGACACATGAAGAAAGAAAGAGATTAAGTCGCGTAT 152
Db      222 GAATCTTGAACACGTAAACCTAGCAGCAGACACATGAAGAAAGAGATTAAGTCGCGTAT 281
QY      153 TGTGAAGAAGACATTAAGAGACACATGTAAGTGGAAATGTAAAGCGCGAAAGTAACCTT 212
Db      282 TGTGAAGAAGACATTAAGAGACACATGTAAGTGGAAATGTAAAGCGCGAAAGTAACCTT 341
QY      213 ATGCATTGTGAATTT 227
Db      342 ATCAACAAGGAATCT 356

RESULT 3
US-09-673-274B-20
: Sequence 20, Application US/09673274B
: GENERAL INFORMATION:
:   APPLICANT: Lamberty, Mireille
:   APPLICANT: Bulet, Phillipe
:   APPLICANT: Brookhart, Gary
:   APPLICANT: Hoffman, Jules
:   TITLE OF INVENTION: GENE CODING FOR HELIOMICINE, AND USE THEREOF
:   FILE REFERENCE: A33595-PCT-USA (0726667.0166)
:   CURRENT APPLICATION NUMBER: US/09/673.274B
:   PRIOR FILING DATE: 1999-04-12
:   PRIOR APPLICATION NUMBER: PCT/FR99/00843
:   PRIOR FILING DATE: 1999-04-12
:   PRIOR APPLICATION NUMBER: FR 98 04933
:   PRIOR FILING DATE: 1998-04-15
:   NUMBER OF SEQ ID NOS: 48
:   SOFTWARE: FastSeq for Windows Version 4.0
:   SEQ ID NO 20
:   LENGTH: 1036
:   TYPE: DNA

```

```

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
FEATURE:
NAME/KEY: promoter
LOCATION: (7)...(532)
FEATURE:
NAME/KEY: CDS
LOCATION: (539)...(736)
FEATURE:
NAME/KEY: terminator
LOCATION: (767)...(1030)
US-09-673-274B-20

Query Match      30.7%   Score 120.6;   DB: 6;   Length 1036;
Best Local Similarity 93.3%   Pred. No. 1.5e-25;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      93  GAATTTGGAAGCGTAAACGACTGACGACAAACAATTAAGAAAGAAAGATTAAGGTGGTGAT 152
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      222  GAATCTTGAAGACGTAAACGACTGACGACAAACAATTAAGAAAGAAAGATTAAGGTGGTGAT 281

QY      153  TGTGAAGAAGACATTAAGAGAGACACATGTAAAGGTGAAAAATGTAAAGGCGGAAAGTAACCTT 212
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      282  TGTGAAGAAGACATTAAGAGAGACACATGTAAAGGTGAAAAATGTAAAGGCGGAAAGTAACCTT 341

QY      213  ATGCATTTGTAAATT 227
      || | ||| |
Db      342  ATCAACAAGGAATCT 356

```

```

RESULT 4
US-09-949-016-13294
; Sequence 13294, Application US/09949016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIORITY FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ. ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13294
LENGTH: 250715
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(250715)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13294

Query Match          10.1%; Score 39.8; DB 7; Length 250715;
Best Local Similarity 52.0%; Pred. No. 0.62;
Matches 89; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

OY      119 ACAACATGAAAGACAGATAGCTCGGTGATTGTGAAGACACATRAGACACATG 178
Db 146653 AGAAGAAGGAGGAAGAAAGAAAGAACGAGAGAGAGAAAGGAAGGAAGAAGA 146712

OY      179 TAAGTGGAAAATGTAAAGGCGGAAGTAACCTTATGCATTGTGTAATTGGTTACGACTA 238
Db 146713 AAAAGAAAGAAACCTTCATCATATGAAAAATAAATTAATTCAGATTATTTATCTTGATTA 146772

OY      239 GTGATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTACGTAGGGA 289

```



Db 146773 ATGTGTGATGCGTGATACACAGATAAATAAATAAATAAAGA 146823

## RESULT 5

US-10-380-935-30  
; Sequence 30, Application US/10380935  
; GENERAL INFORMATION:  
; APPLICANT: WARNER, Simon, Anthony, James  
; APPLICANT: HARKES, Timothy, Robert  
; APPLICANT: ANDREWS, Christopher, John  
; TITLE OF INVENTION: HERBICIDE RESISTANT PLANTS  
; FILE REFERENCE: PPD50594/MO  
; CURRENT APPLICATION NUMBER: US/10/380,935  
; CURRENT FILING DATE: 2003-03-19  
; PRIOR APPLICATION NUMBER: GB0023911.1  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: GB0027693.1  
; PRIOR FILING DATE: 2000-11-13  
; PRIOR APPLICATION NUMBER: GB0023910.3  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 30  
; LENGTH: 309  
; TYPE: DNA  
; ORGANISM: Cauliflower Mosaic Virus  
; FEATURE:  
; OTHER INFORMATION: Enhancer  
US-10-380-935-30

## Query Match

Best Local Similarity 9.9%; Score 39; DB 8; Length 309;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 296  
Db 242 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 280

## RESULT 6

US-10-380-935-37  
; Sequence 37, Application US/10380935  
; GENERAL INFORMATION:  
; APPLICANT: WARNER, Simon, Anthony, James  
; APPLICANT: HARKES, Timothy, Robert  
; APPLICANT: ANDREWS, Christopher, John  
; TITLE OF INVENTION: HERBICIDE RESISTANT PLANTS  
; FILE REFERENCE: PPD50594/MO  
; CURRENT APPLICATION NUMBER: US/10/380,935  
; CURRENT FILING DATE: 2003-03-19  
; PRIOR APPLICATION NUMBER: GB0023911.1  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: GB0027693.1  
; PRIOR FILING DATE: 2000-11-13  
; PRIOR APPLICATION NUMBER: GB0023910.3  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 37  
; LENGTH: 522  
; TYPE: DNA  
; ORGANISM: Figwort Mosaic Virus  
; FEATURE:  
; OTHER INFORMATION: Enhancer  
US-10-380-935-37

## Query Match

Best Local Similarity 9.9%; Score 39; DB 8; Length 522;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 296  
Db 459 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 497

RESULT 7  
US-10-391-414-10  
; Sequence 10, Application US/10391414  
; GENERAL INFORMATION:  
; APPLICANT: SHINOZAKI, Kazuko  
; APPLICANT: KATSUMURA, Koji  
; APPLICANT: ITO, Yusuke  
; TITLE OF INVENTION: Stress Induced Promoter Derived From Rice  
; FILE REFERENCE: 382.1041  
; CURRENT APPLICATION NUMBER: US/10/391,414  
; CURRENT FILING DATE: 2003-03-18  
; PRIOR APPLICATION NUMBER: JP 2002-377316  
; PRIOR FILING DATE: 2002-12-26  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 835  
; TYPE: DNA  
; ORGANISM: Cauliflower mosaic virus  
US-10-391-414-10

## Query Match

Best Local Similarity 9.9%; Score 39; DB 8; Length 835;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 296  
Db 729 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 767

## RESULT 8

US-60-434-166-147  
; Sequence 147, Application US/60434166  
; GENERAL INFORMATION:  
; APPLICANT: Mendel Biotechnology  
; APPLICANT: Creelman, Robert A.  
; APPLICANT: Haake, Volker  
; APPLICANT: Ratcliffe, Oliver  
; APPLICANT: Heard, Jacqueline E.  
; APPLICANT: Adam, Luc J.  
; APPLICANT: Jiang, Cai-Zhong  
; APPLICANT: Reuber, T. Lynne  
; APPLICANT: Riechmann, Jose Luis  
; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS  
; FILE REFERENCE: MBI-0051 P  
; CURRENT APPLICATION NUMBER: US/60/434,166  
; CURRENT FILING DATE: 2002-12-17  
; NUMBER OF SEQ ID NOS: 559  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 147  
; LENGTH: 1683  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; OTHER INFORMATION: G2227  
US-60-434-166-147

## Query Match

Best Local Similarity 9.9%; Score 39; DB 11; Length 1683;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 296  
Db 9 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 47

## RESULT 9

US-10-302-267-1  
; Sequence 1, Application US/10302267  
; GENERAL INFORMATION:

```
; OTHER INFORMATION: Sequence of recombinant construct expressing BGL1 protein
US-10-130-150-13
Query Match          9.9%; Score 39; DB 9; Length 2361;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACGCTAGGATGACGCA 296
DB 113 GATTGATGATATCTCCACGCTAGGATGACGCA 151

RESULT 10
US-10-130-150-13
; Sequence 13, Application US/10130150
; GENERAL INFORMATION:
; APPLICANT: Shoseyov, Oded
; TITLE OF INVENTION: ASPERGILLUS NIGER BETA-GLUCOSIDASE GENE, PROTEIN AND USES THEREOF
; FILE REFERENCE: 02/23831
; CURRENT APPLICATION NUMBER: US/10/130,150
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 3212
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
```

```
; OTHER INFORMATION: Sequence of recombinant construct expressing BGL1 protein
US-10-130-150-13
Query Match          9.9%; Score 39; DB 9; Length 3212;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACGCTAGGATGACGCA 296
DB 197 GATTGATGATATCTCCACGCTAGGATGACGCA 235

RESULT 11
US-10-130-150-18
; Sequence 18, Application US/10130150
; GENERAL INFORMATION:
; APPLICANT: Shoseyov, Oded
; TITLE OF INVENTION: ASPERGILLUS NIGER BETA-GLUCOSIDASE GENE, PROTEIN AND USES THEREOF
; FILE REFERENCE: 02/23831
; CURRENT APPLICATION NUMBER: US/10/130,150
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 3288
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of recombinant construct expressing BGL1 protein fuse
US-10-130-150-18
Query Match          9.9%; Score 39; DB 9; Length 3288;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACGCTAGGATGACGCA 296
DB 197 GATTGATGATATCTCCACGCTAGGATGACGCA 235

RESULT 12
US-10-130-150-15
; Sequence 15, Application US/10130150
; GENERAL INFORMATION:
; APPLICANT: Shoseyov, Oded
; TITLE OF INVENTION: ASPERGILLUS NIGER BETA-GLUCOSIDASE GENE, PROTEIN AND USES THEREOF
; FILE REFERENCE: 02/23831
; CURRENT APPLICATION NUMBER: US/10/130,150
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 3329
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of recombinant construct expressing BGL1 protein fuse
US-10-130-150-15
Query Match          9.9%; Score 39; DB 9; Length 3329;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACGCTAGGATGACGCA 296
DB 197 GATTGATGATATCTCCACGCTAGGATGACGCA 235

RESULT 13
US-10-160-764-40
; Sequence 40, Application US/10160764
```

```

; GENERAL INFORMATION:
; APPLICANT: Huang, Yafan
; APPLICANT: Chailfoux, Maryse
; APPLICANT: Wang, Yang
; APPLICANT: Kuzma, Monika Maria
; APPLICANT: Gilley, Angela Patricia
; TITLE OF INVENTION: Compositions and Methods of Increasing Stress Tolerance
; TITLE OF INVENTION: in Plants
; FILE REFERENCE: 22542-008
; CURRENT APPLICATION NUMBER: US/10/160,764
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,766
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/348,909
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 5247
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
; OTHER INFORMATION: pBI121-35S-AtFTa
US-10-160-764-40

Query Match          9.9%; Score 39; DB 9; Length 5247;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 296
DB 3209 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 3247

RESULT 14
US-10-160-764-4
; Sequence 4, Application US/10160764
; GENERAL INFORMATION:
; APPLICANT: Huang, Yafan
; APPLICANT: Chailfoux, Maryse
; APPLICANT: Wang, Yang
; APPLICANT: Kuzma, Monika Maria
; APPLICANT: Gilley, Angela Patricia
; TITLE OF INVENTION: Compositions and Methods of Increasing Stress Tolerance
; TITLE OF INVENTION: in Plants
; FILE REFERENCE: 22542-008
; CURRENT APPLICATION NUMBER: US/10/160,764
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,766
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/348,909
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 5250
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
; OTHER INFORMATION: pBI121-35S-anti-AtFTa sequence
US-10-160-764-4

Query Match          9.9%; Score 39; DB 9; Length 5250;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 296
DB 3209 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 3247
```

```

RESULT 15
US-10-160-764-48
; Sequence 48, Application US/10160764
; GENERAL INFORMATION:
; APPLICANT: Huang, Yafan
; APPLICANT: Chailfoux, Maryse
; APPLICANT: Wang, Yang
; APPLICANT: Kuzma, Monika Maria
; APPLICANT: Gilley, Angela Patricia
; TITLE OF INVENTION: Compositions and Methods of Increasing Stress Tolerance
; TITLE OF INVENTION: in Plants
; FILE REFERENCE: 22542-008
; CURRENT APPLICATION NUMBER: US/10/160,764
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,766
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/348,909
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 5511
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
; OTHER INFORMATION: pBI121-35S-Anti-AtFTa
US-10-160-764-48

Query Match          9.9%; Score 39; DB 9; Length 5511;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 296
DB 3209 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 3247
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Search completed: April 14, 2003, 12:27:28  
Job time : 407.159 secs



GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 06:53:52 ; Search time 913.489 Seconds  
(without alignments)  
6967.603 Million cell updates/sec

Title: US-09-963-803-19  
Perfect score: 393  
Sequence: 1 aagctgcacgcctgcagca.....cacacacactagagatcc 393

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estln:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 42.4  | 10.8        | 224    | 17 | BH746858 SALK_0036 |
| 2          | 42.4  | 10.8        | 561    | 13 | BM162517 EST565040 |
| 3          | 41    | 10.4        | 222    | 13 | BM161725 EST564248 |
| 4          | 40.2  | 10.2        | 528    | 9  | AL369550 MBLA31610 |
| 5          | 40    | 10.2        | 911    | 17 | AZ548969 ENTEN277F |
| 6          | 39.2  | 10.0        | 480    | 17 | BH639017 1008026H0 |

|    |    |     |     |    |                    |
|----|----|-----|-----|----|--------------------|
| 7  | 39 | 9.9 | 112 | 17 | BH751161 SALK_0494 |
| 8  | 39 | 9.9 | 142 | 17 | BH749349 SALK_0477 |
| 9  | 39 | 9.9 | 153 | 17 | BH619283 SALK_0407 |
| 10 | 39 | 9.9 | 153 | 17 | BH747013 SALK_0080 |
| 11 | 39 | 9.9 | 158 | 17 | BH748291 SALK_0451 |
| 12 | 39 | 9.9 | 165 | 17 | BH747357 SALK_0165 |
| 13 | 39 | 9.9 | 175 | 17 | BH746616 SALK_0452 |
| 14 | 39 | 9.9 | 177 | 17 | BH802465 1008026E1 |
| 15 | 39 | 9.9 | 190 | 17 | BH752801 SALK_0193 |
| 16 | 39 | 9.9 | 193 | 17 | BH748289 SALK_0450 |
| 17 | 39 | 9.9 | 214 | 17 | BH747829 SALK_0353 |
| 18 | 39 | 9.9 | 215 | 17 | BH753813 SALK_0296 |
| 19 | 39 | 9.9 | 219 | 17 | BH747744 SALK_0337 |
| 20 | 39 | 9.9 | 220 | 17 | BH747438 SALK_0174 |
| 21 | 39 | 9.9 | 221 | 17 | BH802415 1008026B0 |
| 22 | 39 | 9.9 | 230 | 17 | BH746474 SALK_0428 |
| 23 | 39 | 9.9 | 230 | 17 | BH799173 1008025B1 |
| 24 | 39 | 9.9 | 237 | 17 | BH802463 1008026E0 |
| 25 | 39 | 9.9 | 244 | 17 | BH746375 SALK_0402 |
| 26 | 39 | 9.9 | 248 | 17 | BH254798 SALK_0172 |
| 27 | 39 | 9.9 | 251 | 17 | BH750171 SALK_0371 |
| 28 | 39 | 9.9 | 254 | 17 | BH748500 SALK_0460 |
| 29 | 39 | 9.9 | 256 | 17 | BH748499 SALK_0460 |
| 30 | 39 | 9.9 | 258 | 17 | BH802470 1008026F0 |
| 31 | 39 | 9.9 | 261 | 17 | BH802493 1008026F0 |
| 32 | 39 | 9.9 | 268 | 17 | BH611919 SALK_0318 |
| 33 | 39 | 9.9 | 269 | 17 | BH211646 SALK_0064 |
| 34 | 39 | 9.9 | 269 | 17 | BH802489 1008026G0 |
| 35 | 39 | 9.9 | 271 | 17 | BH799178 1008025C0 |
| 36 | 39 | 9.9 | 272 | 17 | BH802428 1008026C0 |
| 37 | 39 | 9.9 | 274 | 17 | BH802495 1008026H0 |
| 38 | 39 | 9.9 | 279 | 17 | BH748475 SALK_0460 |
| 39 | 39 | 9.9 | 281 | 17 | BH750170 SALK_0371 |
| 40 | 39 | 9.9 | 281 | 17 | BH802443 1008026D0 |
| 41 | 39 | 9.9 | 284 | 17 | BH213307 SALK_0090 |
| 42 | 39 | 9.9 | 284 | 17 | BH746665 SALK_0457 |
| 43 | 39 | 9.9 | 286 | 17 | BH747007 SALK_0078 |
| 44 | 39 | 9.9 | 293 | 17 | BH610310 SALK_0085 |
| 45 | 39 | 9.9 | 296 | 17 | BH213532 SALK_0093 |

## ALIGNMENTS

RESULT 1  
BH746858 224 bp DNA linear GSS 27-FEB-2002  
SALK\_003694.51.40.x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_003694.51.40.x, DNA sequence.

ACCESSION BH746858  
VERSION BH746858.1 GI:18959973  
KEYWORDS GSS.

SOURCE thale cress.  
ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 224)  
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadriab,  
C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Predelis,L., Shinn,P.,  
Zimmerman,J., and Ecker,J.R.

TITLE A Sequence-indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
JOURNAL Unpublished (2001)  
COMMENT Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of



adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybridZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybridZAP vector and plasmid DNA isolated."

BASE COUNT 99 a 25 c 38 g 60 t  
ORIGIN

Query Match 10.4%; Score 41; DB 13; Length 222;

Best Local Similarity 53.4%; Pred. No. 1.9;

Matches 86; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 88 TGGCGAATTTGAAGACGCTAGACACATGCAATGAAAAGAAAGATAGGTCG 147

DB 10 TGTAAAAGATAGATATATATATACACACAGCTGCTGAAAATGCGAAATGCG 69

QY 148 GTGATTTGTGAAGACATGAGACACATGTAAGTGAAATGTAAGGCGGAAAGTA 207

DB 70 GAATTTATGAAAATGGCTGACAGGTACATAAATGAAATCAATCAAGTCGAAATGA 129

QY 208 ACCTTATGCATTGTGTAATTTGTTAGACATGATGATTGATG 248

DB 130 GGGCGAAGCAATCATATATATTTATGCTTATTTATTTATG 170

## RESULT 4

AL369550

LOCUS

DEFINITION MTBA31G10R1 MTBA Medicago truncatula cDNA clone MTBA31G10 T7, mRNA

ACCESSION AL369550

VERSION AL369550.1 GI:9669303

KEYWORDS

SOURCE

ORGANISM

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.

1 (bases 1 to 528)

Journet,E.P., Crespeau,H., van-Tuinen,D., Gouzy,J., Jaillon,O., Nlebel,A., Carreau,V., Chataigner,O., Kahn,D., Gianlinazzi-Pearson

,V. and Gamas,P.

Medicago truncatula ESTs from nitrogen-starved roots

Unpublished (2000)

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de

Biologie Moleculaire des Relations Plantes-Microorganismes,

CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :

Etienne-Pascal.Journet@inra.fr Website :

http://sequence.toulouse.inra.fr/Mtruncatula.html).

Location/Qualifiers

## FEATURES

source

1..528

/organism="Medicago truncatula"

/cultivar="Jemalong"

/db\_xref="taxon:3880"

/clone="MTBA31G10"

/clone\_lib="MTBA"

/issue\_type="root tips"

/dev\_stage="harvested after 3 days of N-starvation"

/note="Vector: pBluescript pSK; Site\_1: EcoRI; Site\_2:

XhoI; Plants were grown in an aeroponic chamber for 14

days on nitrogen-rich medium followed by 3 days on N-free

medium. RNA was extracted from root tips (1-3 cm). cDNA

was prepared from polyA+ enriched RNA. The cDNA was

directionally ligated into Uni-ZapXR vector from

Stratagene and packaged using Gigapack Gold packaging

extracts. Plasmids containing cDNA inserts were

mass-excised from phage stocks using ExsacII helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France)."

BASE COUNT 173 a 50 c 136 g 169 t  
ORIGIN

Query Match 10.2%; Score 40.2; DB 9; Length 528;

Best Local Similarity 47.1%; Pred. No. 3.5; 138; Indels 0; Gaps 0;

Matches 123; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

QY 129 AAGAGAGATGATAGTCCGTGATTTGAAAGACATAGAGACATAGTAGGAA 188

DB 254 AAGACTTGATGATAGATGTTCTCATGATAGATATATATCATTTGAAGCGTAAAG 313

QY 189 AATGTAAGGCGGAAAGTAACCTTATGATTTGTAATTTGGTTACAGATGATGATG 248

DB 314 AATTTGATTTGATTTAATTTAAGGCTTTCATTTCAATATATGTTGGCAAGCTAATATG 373

QY 249 TGATTCAGATGATGATGATATCTCCACAGCTAAGGATGACGATGCCAGTTAC 308

DB 374 TGAGAAAGATATGAGGTTTATCTCAAAATAAATGTTGTTTATGTTGCTCTGTT 433

QY 309 CGGTATGCCGCTCCCAAGCTTATTTCTTATTTAAGCACTTGTAGTAGCTTAGAA 368

DB 434 GTAGACATTTATTTGATATCAGTATCATTAATTAATTAATTTGATATATATAA 493

QY 369 ACCAACACAAACACCTTAGAG 389

DB 494 AAAAAAAAAAAAACTCGAGG 514

## RESULT 5

A2548969

LOCUS

DEFINITION ENTME27TF Entamoeba histolytica Sheared DNA Entamoeba histolytica

genomic, DNA sequence.

ACCESSION A2548969

VERSION A2548969.1 GI:11173098

KEYWORDS

SOURCE

Entamoeba histolytica.

Eukaryota; Entamoebidae; Entamoeba.

1 (bases 1 to 911)

Loftus,B., Van Aken,S. and Fraser,C.

Determination of clone end sequences from Entamoeba histolytica

HMI:IMSS sheared DNA library

Unpublished (2000)

Contact: Brendan J Loftus

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 3543

Email: b1loftus@igf.org

Clones are derived from the Entamoeba histolytica HMI:IMSS sheared

DNA library

Seq primer: M13-Forward

Class: Shotgun

High quality sequence start: 33

High quality sequence stop: 784.

Location/Qualifiers

## FEATURES

source

1..911

/organism="Entamoeba histolytica"

/strain="HMI:IMSS"

/db\_xref="taxon:5759"

/clone\_lib="Entamoeba histolytica Sheared DNA"

/note="Vector: pROSI; Site\_1: Bst I; Constructed at the

Institute for Genomic Research (TIGR), Rockville, MD.

Genomic DNA isolated from broth cultures of E. histolytica

using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a





RESULT 8  
BH749349  
LOCUS  
DEFINITION  
142 bp DNA linear GSS 27-FEB-2002  
SALK\_047736.48.15.x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_047736.48.15.x, DNA  
sequence.  
ACCESSION  
BH749349  
VERSION  
BH749349.1 GI:18964144  
KEYWORDS  
GSS.  
SOURCE  
thale cress.  
ORGANISM  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 142)  
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadriab  
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,  
Zimmerman,J. and Ecker,J.R.  
A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of  
TDNA.  
Class: TDNA tagged.  
FEATURES  
source  
Location/Qualifiers  
1..142  
/organism="Arabidopsis thaliana"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_047736.48.15.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"  
BASE COUNT  
41 a 36 c 30 g 35 t  
ORIGIN  
Query Match 9.9%; Score 39; DB 17; Length 142;  
Best Local Similarity 100.0%; Pred. No. 6.2; 0; Indels 0; Gaps 0;  
Matches 39; Conservative 0; Mismatches 0;  
QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACCA 296  
|||||  
Db 33 GATTGATGTGATATCTCCACTGACGTAAAGGATGACCA 71  
|||||  
RESULT 9  
BH619283/c  
LOCUS  
DEFINITION  
153 bp DNA linear GSS 30-JAN-2002  
SALK\_040762 Arabidopsis thaliana TDNA insertion lines Arabidopsis  
thaliana genomic clone SALK\_040762, DNA sequence.  
ACCESSION  
BH619283  
VERSION  
BH619283.1 GI:18429799  
KEYWORDS  
GSS.  
SOURCE  
thale cress.  
ORGANISM  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 153)  
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadriab

,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,  
Zimmerman,J. and Ecker,J.R.  
A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of  
TDNA.  
Class: TDNA tagged.  
FEATURES  
source  
Location/Qualifiers  
1..153  
/organism="Arabidopsis thaliana"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_040762"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"  
BASE COUNT  
36 a 34 c 36 g 47 t  
ORIGIN  
Query Match 9.9%; Score 39; DB 17; Length 153;  
Best Local Similarity 100.0%; Pred. No. 6.3; 0; Indels 0; Gaps 0;  
Matches 39; Conservative 0; Mismatches 0;  
QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACCA 296  
|||||  
Db 110 GATTGATGTGATATCTCCACTGACGTAAAGGATGACCA 72  
|||||  
RESULT 10  
BH747013  
LOCUS  
DEFINITION  
153 bp DNA linear GSS 27-FEB-2002  
SALK\_008070.43.05.x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_008070.43.05.x, DNA  
sequence.  
ACCESSION  
BH747013  
VERSION  
BH747013.1 GI:18960128  
KEYWORDS  
GSS.  
SOURCE  
thale cress.  
ORGANISM  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 153)  
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadriab  
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,  
Zimmerman,J. and Ecker,J.R.  
A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of  
TDNA.  
Class: TDNA tagged.  
FEATURES  
source  
Location/Qualifiers  
1..153

```

/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_008070.43.05.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna-protocols.html"

BASE COUNT      47 a      37 c      33 g      36 t

ORIGIN

Query Match      9.9%: Score 39; DB 17; Length 153;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 258 GATTGATGATATCTCCACTGACGTAAAGGATGACGA 296
      |||||||
Db 44 GATTGATGATATCTCCACTGACGTAAAGGATGACGA 82

RESULT 11
BH748291/c 158 bp DNA linear GSS 27-FEB-2002
LOCUS SALK_045100.51.10.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_045100.51.10.x, DNA
sequence.
ACCESSION BH748291 GI:18961648
VERSION BH748291.1
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 158)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadlinab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
FEATURES
source Location/Qualifiers
1..158
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_045100.51.10.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna-protocols.html"

BASE COUNT      37 a      35 c      37 g      49 t

ORIGIN

Query Match      9.9%: Score 39; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 258 GATTGATGATATCTCCACTGACGTAAAGGATGACGA 296
      |||||||
Db 110 GATTGATGATATCTCCACTGACGTAAAGGATGACGA 72

RESULT 12
BH747357 165 bp DNA linear GSS 27-FEB-2002
LOCUS SALK_016522.55.50.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_016522.55.50.x, DNA
sequence.
ACCESSION BH747357 GI:18960472
VERSION BH747357
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 165)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadlinab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
FEATURES
source Location/Qualifiers
1..165
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_016522.55.50.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna-protocols.html"

BASE COUNT      45 a      43 c      39 g      38 t

ORIGIN

Query Match      9.9%: Score 39; DB 17; Length 165;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 258 GATTGATGATATCTCCACTGACGTAAAGGATGACGA 296
      |||||||
Db 34 GATTGATGATATCTCCACTGACGTAAAGGATGACGA 72

RESULT 13
BH746616 175 bp DNA linear GSS 27-FEB-2002
LOCUS SALK_045268.54.50.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_045268.54.50.x, DNA
sequence.
ACCESSION BH746616 GI:18959731
VERSION BH746616
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana

```

REFERENCE  
AUTHORS

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsids. 1 (bases 1 to 175)

## TITLE

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.  
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL  
COMMENT

Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: eckersalk.edu

This is single pass sequence recovered from the left border of TDNA.

## FEATURES

## source

Class: TDNA tagged.  
Location/Qualifiers

1..175  
/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_045268.54.50.x"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/cdna\\_protocols.html](http://signal.salk.edu/cdna_protocols.html)"

BASE COUNT  
ORIGIN

54 a 43 c 40 g 38 t

## Query Match

9.9%; Score 39; DB 17; Length 175;

Best Local Similarity 100.0%; Pred. No. 6.4; Mismatches 0; Indels 0; Gaps 0;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14  
BH802465/c

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

BH802465 177 bp DNA linear GSS 25-APR-2002  
1008026E10.y2 1008 - RescueMu Grid I Zea mays genomic, DNA sequence.  
BH802465  
BH802465.1 GI:20316614  
GSS.  
Zea mays.  
Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 177)  
Walbot,V.  
Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu

Very probable ligation site found so sequence was trimmed.  
Post-ligation sequence submitted separately.  
Plate: 1008026 row: 10  
Class: transposon-tagged.

## FEATURES

## source

Location/Qualifiers  
1..177

/organism="Zea mays"

/cultivar="mixed background W23/A188/B73"

/db\_xref="taxon:4577"

/clone.lib="1008 - RescueMu Grid I"

/tissue-type="leaf"

/dev\_stage="adult"

/lab\_host="DH10B"

/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site\_1: BamHI; Site\_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site [www.zmld.laestate.edu](http://www.zmld.laestate.edu) and follow the links for 'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT  
ORIGIN

39 a 38 c 47 g 53 t

Query Match  
Best Local Similarity 100.0%; Pred. No. 6.4; Mismatches 0; Indels 0; Gaps 0;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15  
BH752801

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

BH752801 190 bp DNA linear GSS 27-FEB-2002  
SALK\_019366.54.25.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK\_019366.54.25.x, DNA sequence.  
BH752801  
BH752801.1 GI:18972023  
GSS.  
thale cress.  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsids. 1 (bases 1 to 190)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.  
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: eckersalk.edu

This is single pass sequence recovered from the left border of TDNA.  
Class: TDNA tagged.  
Location/Qualifiers

FEATURES  
source

1..190  
/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_019366.54.25.x"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html).

BASE COUNT

52 a 52 c 41 g 45 t

ORIGIN

Query Match

9.9%; Score 39; DB 17; Length 190;

Best Local Similarity 100.0%; Pred. No. 6.4;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAAGGATGACGCA 296  
|||||  
Db 81 GATTGATGATATCTCCACTGACGTAAGGATGACGCA 119

Search completed: April 14, 2003, 10:25:42  
Job time : 916.489 secs

GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 04:10:42 ; Search time 1319.64 Seconds

(without alignments)  
10188.783 Million cell updates/sec

Title: US-09-963-803-20

Perfect score: 462  
Sequence: 1 aagcttgatgctgcgcagca.....cacacaacctagagatcc 462

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_da:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_on:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rtd:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 462   | 100.0       | 462    | 6     | AX036754    |
| 2          | 373.6 | 80.9        | 600    | 6     | AX036756    |
| 3          | 364.6 | 78.9        | 9285   | 6     | AX093047    |
| 4          | 364.6 | 78.9        | 15077  | 6     | AX093052    |
| 5          | 354.2 | 76.7        | 541    | 6     | AX036758    |
| 6          | 314   | 68.0        | 393    | 6     | AX036753    |
| 7          | 262   | 56.7        | 604    | 6     | AX036757    |
| 8          | 240.2 | 52.0        | 392    | 6     | AX036755    |
| 9          | 212.4 | 46.0        | 317    | 6     | AX036737    |
| 10         | 212.4 | 46.0        | 472    | 6     | AX036738    |
| 11         | 200.4 | 43.4        | 348    | 6     | AX036739    |
| 12         | 152.8 | 33.1        | 371    | 6     | AX036736    |
| 13         | 140.8 | 30.5        | 301    | 6     | AX036741    |
| 14         | 140.8 | 30.5        | 398    | 6     | AX036740    |
| 15         | 120.6 | 26.1        | 515    | 6     | AX036736    |
| 16         | 120.6 | 26.1        | 515    | 6     | AX088388    |
| 17         | 120.6 | 26.1        | 532    | 6     | AX020413    |
| 18         | 120.6 | 26.1        | 838    | 6     | AX014764    |
| 19         | 120.6 | 26.1        | 853    | 6     | AX088389    |
| 20         | 120.6 | 26.1        | 1036   | 6     | AX014765    |
| 21         | 120.6 | 26.1        | 8158   | 14    | CVU20341    |
| 22         | 120.6 | 26.1        | 8159   | 14    | CVU59751    |
| 23         | 120.6 | 26.1        | 8340   | 6     | AX329231    |
| 24         | 120.6 | 26.1        | 8340   | 6     | AX338536    |
| 25         | 120.6 | 26.1        | 12241  | 6     | AX412168    |
| 26         | 115.8 | 25.1        | 593    | 6     | AX088390    |
| 27         | 115.8 | 25.1        | 857    | 6     | AX088391    |
| 28         | 115.8 | 25.1        | 931    | 6     | AX088392    |
| 29         | 115.4 | 25.0        | 931    | 6     | AX088393    |
| 30         | 115.4 | 25.0        | 931    | 6     | AX088393    |
| 31         | 81.4  | 17.6        | 7489   | 14    | CTWVCG      |
| 32         | 80    | 17.3        | 243    | 6     | AX036735    |
| 33         | 75.4  | 16.3        | 392    | 6     | AX036755    |
| 34         | 69.6  | 15.1        | 79     | 6     | AX036611    |
| 35         | 69.6  | 15.1        | 79     | 6     | AX036748    |
| 36         | 69.6  | 15.1        | 296    | 6     | AX036603    |
| 37         | 69    | 14.9        | 259    | 6     | AX036616    |
| 38         | 62    | 13.4        | 60     | 6     | AX036743    |
| 39         | 60    | 13.0        | 60     | 6     | AX036743    |
| 40         | 60    | 12.6        | 80     | 6     | AX036746    |
| 41         | 58    | 12.6        | 236    | 6     | AX103783    |
| 42         | 58    | 12.6        | 236    | 6     | AX103783    |
| 43         | 58    | 12.6        | 299    | 6     | AX103784    |
| 44         | 58    | 12.6        | 332    | 6     | AX103755    |
| 45         | 58    | 12.6        | 472    | 6     | AX103753    |

#### ALIGNMENTS

RESULT 1  
AX036754  
LOCUS AX036754  
DEFINITION Sequence 20 from Patent WO0058485.  
ACCESSION AX036754  
VERSION AX036754.1 GI:11226263  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct.  
artificial construct.  
REFERENCE  
1 (bases 1 to 462)  
Rance, I., Theisen, M. and Gruber, V.  
Chimeric expression promoters originating from commelina yellow  
mottle virus and cassava vein mosaic virus  
TITLE  
JOURNAL  
Patent: WO 0058485-A 20 05-Oct-2000;



OY 130 AAGAAGATTAAGGTCGATTTGTGAAGAGCATAGAGACATTAAGTGAAGAA 189  
|||||  
Db 5919 AAGAAGATTAAGGTCGATTTGTGAAGAGCATAGAGACATTAAGTGAAGAA 5978  
|||||  
OY 190 ATGAAGGCGGAAAGTAACCTTATGATTTGTTAGGACTAGTATGATGT 249  
|||||  
Db 5979 ATGAAGGCGGAAAGTAACCTTATGATTTGTTAGGACTAGTATGATGT 6038  
|||||  
OY 250 GATATCAAGATTGATGTATATCTCCACTGACGTAAGGAGTACGATGCCACTAGT 309  
|||||  
Db 6039 GATATCAAGATTGATGTATATCTCCACTGACGTAAGGAGTACGATGCCACTAGT 6098  
|||||  
OY 310 GATTGATGTATATCAAGATTGATGTATATCTCCACTGACGTAAGGAGTACGATGCC 369  
|||||  
Db 6099 GATTGATGTATATCAAGATTGATGTATATCTCCACTGACGTAAGGAGTACGATGCC 6158  
|||||  
OY 370 ACGTTACCGGTATGCCGTTCCCAAGCTTATTT 404  
|||||  
Db 6159 ACGACTAGTATGATGTATATCAAGATTGATGT 6193  
|||||

RESULT 4  
AX093052 15077 bp DNA linear PAT 30-MAR-2001  
LOCUS Sequence 57 from Patent W00118192.  
DEFINITION AX093052  
ACCESSION AX093052  
VERSION AX093052.1 GI:13509527  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 15077)  
AUTHORS Gruber, V. and Comeau, D.  
TITLE Synthetic vectors, transgenic plants containing them, and methods for obtaining them  
JOURNAL Patent: WO 0118192-A 57 15-MAR-2001;  
MERISTEM THERAPEUTICS (FR)  
FEATURES  
source location/Qualifiers  
1..15077  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="PMRT1342"  
misc\_feature 1  
/note="PMRT1342 results from the replacement of the expression cassette ep355-gus-polyA35S from PMRT1335 by the expression cassette L5-gus-polyA35S isolated from PMRT1336"

BASE COUNT 3672 a 3892 c 4225 g 3288 t  
ORIGIN

Query Match 78.98; Score 364.6; DB 6; Length 15077;  
Best Local Similarity 95.2%; Pred. No. 1.5e-89;  
Matches 376; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 10 TGGCTGAGCACTAGTATCCGCGTCATCATGACATCATACAGTACTGAGAGTGA 69  
|||||  
Db 6838 TGGCTGAGCACTAGTATCCGCGTCATCATGACATCATACAGTACTGAGAGTGA 6897  
|||||  
OY 70 TAGTACCATGACACTCTGTGCAATATTTGAAGACGTAACACTGACGACAAATGAA 129  
|||||  
Db 6898 TAGTACCATGACACTCTGTGCAATATTTGAAGACGTAACACTGACGACAAATGAA 6957  
|||||  
OY 130 AAGAAGATTAAGTGGTGGTATTTGTAAGAGACATAGAGACATGTAAGTGA 189  
|||||  
Db 6958 AAGAAGATTAAGTGGTGGTATTTGTAAGAGACATAGAGACATGTAAGTGA 7017  
|||||  
OY 190 ATGAAGGCGGAAAGTAACCTTATGATTTGTTAGGACTAGTATGATGT 249  
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Db 7018 ATGAAGGCGGAAAGTAACCTTATGATTTGTTAGGACTAGTATGATGT 7077  
|||||  
OY 250 GATATCAAGATTGATGTATATCTCCACTGACGTAAGGAGTACGATGCCACTAGT 309  
|||||

Db 7078 GATATCAAGATTGATGTATATCTCCACTGACGTAAGGAGTACGATGCCACTAGT 7137  
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OY 310 GATTGATGTATATCAAGATTGATGTATATCTCCACTGACGTAAGGAGTACGATGCC 369  
|||||  
Db 7138 GATTGATGTATATCAAGATTGATGTATATCTCCACTGACGTAAGGAGTACGATGCC 7197  
|||||  
OY 370 ACGTTACCGGTATGCCGTTCCCAAGCTTATTT 404  
|||||  
Db 7198 ACGACTAGTATGATGTATATCAAGATTGATGT 7232  
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RESULT 5  
AX036758 541 bp DNA linear PAT 16-NOV-2000  
LOCUS Sequence 24 from Patent W00058465.  
DEFINITION AX036758  
ACCESSION AX036758  
VERSION AX036758.1 GI:11226267  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 541)  
AUTHORS Rance, I., Theisen, M. and Gruber, V.  
TITLE Chimeric expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus  
JOURNAL Patent: WO 0058465-A 24 05-OCT-2000;  
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)  
FEATURES  
source location/Qualifiers  
1..541  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="promoter Mpr1168"  
promoter 1..541  
BASE COUNT 169 a 104 c 130 g 138 t  
ORIGIN

Query Match 76.78; Score 354.2; DB 6; Length 541;  
Best Local Similarity 98.4%; Pred. No. 1.3e-86;  
Matches 379; Conservative 0; Mismatches 3; Indels 3; Gaps 2;

OY 78 CATGACACTGTGTCGATATTTGAAGACGTAAGCACTGACGACAAATGAAGAA 137  
|||||  
Db 160 CATGCCACTGTGTCGATATTTGAAGACGTAAGCACTGACGACAAATGAAGAA 219  
|||||  
OY 138 GATTAAGTCCGTTGTTGTAAGAGACATAGAGACATGTAAGTGAAGTGAAG 197  
|||||  
Db 220 GATTAAGTCCGTTGTTGTAAGAGACATAGAGACATGTAAGTGAAGTGAAG 278  
|||||  
OY 198 GCGGAAGTAACCTTATGCAATTTGTTAGCACTAGTATGATGTATCA 257  
|||||  
Db 279 GCGGAAGTAACCTTATGCAATTTGTTAGCACTAGTATGATGTATCA 338  
|||||  
OY 258 GATTGATGTATATCTCCACTGACGTAAGGAGTACGATGCCACTAGTATG 317  
|||||  
Db 339 GATTGATGTATATCTCCACTGACGTAAGGAGTACGATGCCACTAGTATG 398  
|||||  
OY 318 TGATATCAAGATTGATGTATATCTCCACTGACGTAAGGAGTACGATGCCACTAGT 377  
|||||  
Db 399 TGATATCAAGATTGATGTATATCTCCACTGACGTAAGGAGTACGATGCCACTAGT 458  
|||||  
OY 378 CGGATGCCGGTCCCAAGCTTTATTTGTTAAGCACTGTGTAGTGA 437  
|||||  
Db 459 CGGATGCCGGTCCCAAGCTTTATTTGTTAAGCACTGTGTAGTGA 516  
|||||  
OY 438 ACCAACAACAACCTAGAGATCC 462  
|||||  
Db 517 ACCAACAACAACCTAGAGATCC 541  
|||||

RESULT 6  
AX036753 393 bp DNA linear PAT 16-NOV-2000  
LOCUS AX036753

| DEFINITION                | Sequence 19 from Patent WO0058485.   |
|---------------------------|--|
| ACCESSION                 | AX036753   |
| VERSION                   | AX036753.1 GI:11226262   |
| KEYWORDS                  | synthetic construct.   |
| SOURCE                    | synthetic construct  |
| ORGANISM                  | artificial sequences.  |
| REFERENCE                 | 1 (bases 1 to 393)   |
| AUTHORS                   | Range, I., Theisen, M., and Gruber, V.   |
| TITLE                     | Chimeric expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus |
| JOURNAL                   | Patent: WO 0058485-A 19 05-Oct-2000;   |
|                           | MEISENUM THERAPEUTICS (FR) ; RANGE IANN (FR) ; THEISEN MANFRED (FR)  |
| FEATURES                  | ;  |
| source                    | Location/Qualifiers  |
|                           | 1..393   |
|                           | /organism="synthetic construct"  |
|                           | /db_xref="taxon:32630"   |
|                           | /note="promoter Mp1162"  |
|                           | 1..393   |
| PROMOTER                  | 128 a 75 c 93 g 97 t   |
| BASE COUNT                |  |
| ORIGIN                    |  |
| Query Match               | 68.0%; Score 314; DB 6; Length 393;  |
| Best Local Similarity     | 85.1%; Pred. No. 1.5e-75;  |
| Matches 393; Conservative | 0; Mismatches 0; Indels 69; Gaps 1;  |
| QY                        | 1 AAGCTTGCATGCGCTGCACACACTAGTATCCGCGTGCATCAATGACATCACTACAGTACTGA 60  |
| DB                        | 1 AAGCTTGCATGCGCTGCACACACTAGTATCCGCGTGCATCAATGACATCACTACAGTACTGA 60  |
| QY                        | 61 GGAGATGAATAGCTAGCCATGACACTCTGTGCGAATATTGAAGACGTAAAGCACTGACGAC 120                                       |
| DB                        | 61 GGAGATGAATAGCTAGCCATGACACTCTGTGCGAATATTGAAGACGTAAAGCACTGACGAC 120                                       |
| QY                        | 121 AACATGAAAAGCAACATAAGTCCGGTGAATGGAAGAAGACATAGAGACACATGTA 180  |
| DB                        | 121 AACATGAAAAGCAACATAAGTCCGGTGAATGGAAGAAGACATAGAGACACATGTA 180  |
| QY                        | 181 AGGTGGAATATGTAAGGCGCGAAGTAACCTTATGCAATTTGGTATTCAGACTAGT 240  |
| DB                        | 181 AGGTGGAATATGTAAGGCGCGAAGTAACCTTATGCAATTTGGTATTCAGACTAGT 240  |
| QY                        | 241 GATGATGATGATATCAAGATTTGATGATATCTCCACTGACGTAAAGGATGACGCGATGCC 300                                       |
| DB                        | 241 GATGATGATGATATCAAGATTTGATGATATCTCCACTGACGTAAAGGATGACGCGATGCC 300                                       |
| QY                        | 301 ACGACTAGTGAATGATGATATCAAGATTTGATGATATCTCCACTGACGTAAAGGATG 360  |
| DB                        | 301 ACGACTAGTGAATGATGATATCAAGATTTGATGATATCTCCACTGACGTAAAGGATG 360  |
| QY                        | 361 ACGCATGCCACGTTACCCGGTATGCGGATGCCAAGCTTTATTTTCCTATTAAACACTT 420   |
| DB                        | 361 ACGCATGCCACGTTACCCGGTATGCGGATGCCAAGCTTTATTTTCCTATTAAACACTT 420   |
| QY                        | 421 GTGTAGTACTAGAAAACCAACACACACACACACCTAGAGATCC 462  |
| DB                        | 421 GTGTAGTACTAGAAAACCAACACACACACACACCTAGAGATCC 462  |
| QY                        | 463 GTGTAGTACTAGAAAACCAACACACACACACCTAGAGATCC 493  |
| DB                        | 463 GTGTAGTACTAGAAAACCAACACACACACACCTAGAGATCC 493  |
| RESULT 7                  |  |
| LOCUS                     | AX036757 604 bp DNA linear PAT 16-NOV-2000   |
| DEFINITION                | Sequence 23 from Patent WO0058485.   |
| ACCESSION                 | AX036757   |
| VERSION                   | AX036757.1 GI:11226266   |
| KEYWORDS                  | synthetic construct.   |
| SOURCE                    | synthetic construct  |
| ORGANISM                  | artificial sequences.  |
| REFERENCE                 | 1 (bases 1 to 604)   |
| AUTHORS                   | Range, I., Theisen, M., and Gruber, V.   |
| TITLE                     | Chimeric expression promoters originating from commelina yellow  |

| JOURNAL                   |   | mottle virus and cassava vein mosaic virus<br>Patent: WO 0058485-A 23 05-OCT-2000;<br>MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)<br>; GRUBER VERONIQUE (FR)<br>Location/Qualifiers |                 |
|---------------------------|---|---|-----------------|
| FEATURES                  |   | 1..604  |                 |
| source                    |   | /organism="synthetic construct"<br>/db_xref="taxon:32630"<br>/note="Promoter MPr1167"   |                 |
| BASE COUNT                |   | 186 a 116 c 145 g 157 t   |                 |
| ORIGIN                    |   |   |                 |
| Query Match               | 56.7%; Score 262; DB 6; Length 604;   |   |                 |
| Best Local Similarity     | 83.3%; Pred. No. 2,86-61;   |   |                 |
| Matches 375; Conservative | 0; Mismatches 5; Indels 70; Gaps 4;   |   |                 |
| OY                        | 78  | CATGCACTCMTGCGATATTGTAAGACGTAAAGCCTGACGACACACATGGAAGAACAA   | 137             |
| DB                        | 160   | CATGCCACTCTGTGGGAATTATTAAGAGCTAAGCCTGACGACACACATGGAAGAACAA  | 219             |
| OY                        | 138   | GATAAGTCGCGGATTTGAAAGAGACATAGAGACACATGTAAAGTGGAATGTAAG  | 197             |
| DB                        | 220   | CATAAGTCGCGGATTTG- AAGAGACATAGAGACACATGTAAAGTGGAATGTAAG   | 278             |
| OY                        | 198   | GCGGAAGTAACCTTATGCAATTTGTAATTTGCTTACGACTAGTATGATGATATCAA  | 257             |
| DB                        | 279   | GCGGAAGTAACCTTATGCAATTTGTAACCTTGTTAC--CTAGTATGATGATGATATCAA   | 336             |
| OY                        | 258   | GATTGATGTGATATCTCCACTGACGTAAAGGGATGACGATGCCA-----   | 301             |
| DB                        | 337   | GATTGATGTGATATCTCCACTGACGTAAAGGGATGACGATGCCACCTAGTATGATGTG  | 396             |
| OY                        | 302   | -----CGACTAGTAT   | 312             |
| DB                        | 397   | ATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGGATGACGATGCCACCTAGTAT   | 456             |
| OY                        | 313   | TGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGGATGACGATGCCACG  | 372             |
| DB                        | 457   | TGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGGATGACGATGCCACG  | 516             |
| OY                        | 373   | TTACCCGCTATGCCGCTTCCCAAGCTTTATTTCCCTTATTTAAAGCCTTGTTAGTACTT   | 432             |
| DB                        | 517   | TTACCCGCTATGCCGCTTCCCAAGCTTTATTTCCCTTATTTAA--ACTTGTGTAGTACTT  | 574             |
| OY                        | 433   | AGAAACCAACACACACACACTAGAGATCC   | 462             |
| DB                        | 575   | AGAAACCAACACACACACACTAGAGATCC   | 604             |
| RESULT 8                  |   |   |                 |
| LOCUS                     | AX036755  | 392 bp  | DNA             |
| DEFINITION                | Sequence 21 from Patent WO0058485.  | Linear  | PAT 16-NOV-2000 |
| ACCESSION                 | AX036755  |   |                 |
| VERSION                   | AX036755.1  | GI:11226264   |                 |
| KEYWORDS                  | .   |   |                 |
| SOURCE                    | synthetic construct.  |   |                 |
| ORGANISM                  | artificial sequences.   |   |                 |
| REFERENCE                 | 1 (bases 1 to 392)  |   |                 |
| AUTHORS                   | Rance,I., Theisen,M. and Gruber,V.  |   |                 |
| TITLE                     | Chimeric expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus  |   |                 |
| JOURNAL                   | Patent: WO 0058485-A 21 05-OCT-2000;<br>MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)<br>; GRUBER VERONIQUE (FR)<br>Location/Qualifiers |   |                 |
| FEATURES                  | 1..392  |   |                 |
| source                    | /organism="synthetic construct"<br>/db_xref="taxon:32630"<br>/note="Promoter MPr1164"   |   |                 |
| 1..392                    |   |   |                 |



[illegible]

|   |  |             |  |        |  |  |  |  |
|---|--|-------------|--|--------|--|--|--|--|
| QY  | 80   | TCACCTCGTGC | AATATTTGAAGACGTGAAGACGTGACACAAACATGAAAGGAACA     | 139    |  |  |  |  |
| Db  | 78   | TCACCTCTGTG | CCGAAATATTGAAAGCGTAGACACTGACACAAACATGAAAAAGGAACA | 137    |  |  |  |  |
| QY  | 140  | TAAGTCGGTGA | TTTGTGAAAGACATAGAGACACATGTAAGTGGAAGATGTAAAGGC    | 199    |  |  |  |  |
| Db  | 138  | TAAGTCGGTGA | TTTGTGAAAGACATAGAGACACATGTAAGTGGAAGATGTAAAGGC    | 197    |  |  |  |  |
| QY  | 200  | GGAAGTAACCT | TATGATTTGTAATTTGGTTAC                            | 233    |  |  |  |  |
| Db  | 198  | GGAAGTAACCT | TATGATTTGTAATTTGGTTAC                            | 231    |  |  |  |  |
| RESULT 10   |  |             |  |        |  |  |  |  |
| LOCUS   | AX036759   | 472 bp      | DNA  | linear |  |  |  |  |
| DEFINITION  | Sequence 25 from Patent WO0058485.   |             |  |        |  |  |  |  |
| ACCESSION   | AX036759   |             |  |        |  |  |  |  |
| VERSION   | AX036759.1   | GI:11226268 |  |        |  |  |  |  |
| KEYWORDS  | synthetic construct.   |             |  |        |  |  |  |  |
| ORGANISM  | synthetic construct.   |             |  |        |  |  |  |  |
| REFERENCE   | artificial sequences.  |             |  |        |  |  |  |  |
| AUTHORS   | 1 (bases 1 to 472)   |             |  |        |  |  |  |  |
| TITLE   | Rance, I.; Theisen, M. and Gruber, V.  |             |  |        |  |  |  |  |
| JOURNAL   | Chimeric expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus |             |  |        |  |  |  |  |
|   | Patent: WO 0058485-A 25 05-02-2000;  |             |  |        |  |  |  |  |
|   | MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)  |             |  |        |  |  |  |  |
| FEATURES  | ; GRUBER VERONIQUE (FR)  |             |  |        |  |  |  |  |
| SOURCE  | location/Qualifiers  |             |  |        |  |  |  |  |
|   | 1..472   |             |  |        |  |  |  |  |
|   | /organism="synthetic construct"  |             |  |        |  |  |  |  |
|   | /db_xref="taxon:32630"   |             |  |        |  |  |  |  |
|   | /note="Promoter Mpr1169"   |             |  |        |  |  |  |  |
| BASE COUNT  | 149 a  | 92 c        | 112 g  | 119 t  |  |  |  |  |
| ORIGIN  | 1..472   |             |  |        |  |  |  |  |
|   | promoter   |             |  |        |  |  |  |  |
| Query Match   |  |             |  |        |  |  |  |  |
| Best Local Similarity 91.5%; Pred. No. 1.2e-47;               |  |             |  |        |  |  |  |  |
| Matches 236; Conservative 0; Mismatches 21; Indels 1; Gaps 1; |  |             |  |        |  |  |  |  |
| QY  | 78   | CATGCACTCTG | TGGGATATTTGAAGACTAGACACTGACGACACAAATGAAAAGAA     | 137    |  |  |  |  |
| Db  | 160  | CATGCACTCTG | TGGGATATTTGAAGACTAGACACTGACGACACAAATGAAAAGAA     | 219    |  |  |  |  |
| QY  | 138  | GATAAGTCGCG | GATTTGCAAAAGACATAGAGACACATGTAAGTGGAATGTAAG       | 197    |  |  |  |  |
| Db  | 220  | GATAAGTCGCG | GATTTGCG - AAGACACATAGAGACACATGTAAGTGGAATGTAAG   | 278    |  |  |  |  |
| QY  | 198  | GCGGAAGTAAC | CTTATGCAATTTGTAATTTGGTTACGACTAGTGTGATGATTCAA     | 257    |  |  |  |  |
| Db  | 279  | GCGGAAGTAAC | CTTATGCAATTTGTAATTTGGTTACGACTAGTGTGATGATTCAA     | 338    |  |  |  |  |
| QY  | 258  | GATGATGTAAT | TCACGTGACGTGAAGGATGAGCATGCGACAGCAGTAGATGTAAG     | 317    |  |  |  |  |
| Db  | 339  | GATGATGTAAT | TCACGTGACGTGAAGGATGAGCATGCGACAGCAGTAGATGTAAG     | 398    |  |  |  |  |
| QY  | 318  | TGATATCAAG  | ATGTGATGTT 335                                   |        |  |  |  |  |
| Db  | 399  | GGTTCACCAAG | CTTATTT 416                                      |        |  |  |  |  |
| RESULT 11   |  |             |  |        |  |  |  |  |
| LOCUS   | AX036738   | 348 bp      | DNA  | linear |  |  |  |  |
| DEFINITION  | Sequence 4 from Patent WO0058485.  |             |  |        |  |  |  |  |
| ACCESSION   | AX036738   |             |  |        |  |  |  |  |
| VERSION   | AX036738.1   | GI:11226247 |  |        |  |  |  |  |
| KEYWORDS  | synthetic construct.   |             |  |        |  |  |  |  |
| SOURCE  | synthetic construct.   |             |  |        |  |  |  |  |

|                       |  |  |               |             |
|-----------------------|--|--|---------------|-------------|
| ORGANISM              | synthetic construct  |  |               |             |
| REFERENCE             | artificial sequences.  |  |               |             |
| AUTHORS               | 1 (bases 1 to 348)   |  |               |             |
| TITLE                 | Rance,I., Theisen,M. and Gruber,V.   |  |               |             |
| JOURNAL               | Chimeric expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus |  |               |             |
|                       | Patent: WO 0058485-A 4 05-OCT-2000;  |  |               |             |
|                       | MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)  |  |               |             |
| FEATURES              | ; GRUBER VERONIQUE (FR)  |  |               |             |
| SOURCE                | Location/Qualifiers  |  |               |             |
|                       | 1..348   |  |               |             |
|                       | /organism="synthetic construct"  |  |               |             |
|                       | /db_xref="taxon:32630"   |  |               |             |
|                       | /note="promoter MPr117"  |  |               |             |
| PROMOTER              | 1..348   |  |               |             |
| BASE COUNT            | 116 a  | 70 c   | 78 g          | 84 t        |
| ORIGIN                |  |  |               |             |
| Query Match           | 43.4%  | Score 200.4;   | DB 6;         | Length 348; |
| Best Local Similarity | 99.1%;   | Pred. No. 2.4e-44;   |               |             |
| Matches               | 212;   | Conservative 0;  | Mismatches 1; | Indels 1;   |
| Gaps                  | 1;   |  |               |             |
| QY                    | 20   | ACTAGTATCCGCCGTCATCATGACATCATCAGCTACTGAGAGATGATAGCTAGCCA     | 79            |             |
| DB                    | 52   | ACTAGTATCCGCCGTCATCATGACATCATCAGCTACTGAGAGATGATAGCTAGCCA     | 111           |             |
| QY                    | 80   | TGACACTCTGTGTCGCAATATTGAAAGCGTAGACACGACACAACATGAAAGAGAGA     | 139           |             |
| DB                    | 112  | TGACACTCTGTGTCGCAATATTGAAAGCGTAGACACGACACAACATGAAAGAGAGA     | 171           |             |
| QY                    | 140  | TAAAGTCGGTGATTTGTGAAGAGACATGAGACACATGTAAGTGGAATAATGTAAGGC    | 199           |             |
| DB                    | 172  | TAAAGTCGGTGATTTGTG-AAGAGACATGAGAGACACATGTAAGTGGAATAATGTAAGGC | 230           |             |
| QY                    | 200  | GGAAGTAACTTATGATTCATTTTATTTGGTTAC                            | 233           |             |
| DB                    | 231  | GGAAGTAACTTATGATTCATTTGTTACTGGTTAC                           | 264           |             |
| RESULT 12             |  |  |               |             |
| LOCUS                 | AX036739   | 371 bp   | DNA           | linear      |
| DEFINITION            | Sequence 5 from Patent WO0058485.  |  |               |             |
| ACCESSION             | AX036739   |  |               |             |
| VERSION               | AX036739.1   | GI:11226248  |               |             |
| KEYWORDS              | .  |  |               |             |
| SOURCE                | synthetic construct.   |  |               |             |
| ORGANISM              | synthetic construct.   |  |               |             |
| REFERENCE             | artificial sequences.  |  |               |             |
| AUTHORS               | 1 (bases 1 to 371)   |  |               |             |
| TITLE                 | Rance,I., Theisen,M. and Gruber,V.   |  |               |             |
| JOURNAL               | Chimeric expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus |  |               |             |
|                       | Patent: WO 0058485-A 5 05-OCT-2000;  |  |               |             |
|                       | MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)  |  |               |             |
| FEATURES              | ; GRUBER VERONIQUE (FR)  |  |               |             |
| SOURCE                | Location/Qualifiers  |  |               |             |
|                       | 1..371   |  |               |             |
|                       | /organism="synthetic construct"  |  |               |             |
|                       | /db_xref="taxon:32630"   |  |               |             |
|                       | /note="promoter MPr1146"   |  |               |             |
| PROMOTER              | 1..371   |  |               |             |
| BASE COUNT            | 122 a  | 68 c   | 89 g          | 92 t        |
| ORIGIN                |  |  |               |             |
| Query Match           | 33.1%  | Score 152.8;   | DB 6;         | Length 371; |
| Best Local Similarity | 98.7%;   | Pred. No. 2.9e-31;   |               |             |
| Matches               | 154;   | Conservative 0;  | Mismatches 2; | Indels 0;   |
| Gaps                  | 0;   |  |               |             |
| QY                    | 78   | CATGACACCTGTGGGAATATTGAAGACGTAGACACTGACGACACAACATGAAGAAGAA   | 137           |             |
| DB                    | 130  | CATGACACCTGTGTGGGAATATTGAAGACGTAGACACTGACGACACAACATGAAGAAGAA | 189           |             |

|                       |                                   |   |                 |
|-----------------------|-----------------------------------|---|-----------------|
| QY                    | 138                               | GATAAGTCGCGGATTGTGAAAGACACATATAGGACACATGTAAAGTCGAAATGTAAAG  | 197             |
| DB                    | 190                               | GATTAAGTCGCGGATTGTGAAAGACACATATAGGACACATGTAAAGTCGAAATGTAAAG | 249             |
| QY                    | 198                               | GCGGAAGTAACCTTATGCATTGTGTAATTTGGTTAC                        | 233             |
| DB                    | 250                               | GCGGAAGTAACCTTATGCATTGTGTAATTTGGTTAC                        | 285             |
| RESULT 13             |                                   |   |                 |
| LOCUS                 | AX036741                          | 301 bp  | DNA             |
| DEFINITION            | Sequence 7 from Patent WO0058485. |   | Linear          |
| ACCESSION             | AX036741                          |   | PAT 16-NOV-2000 |
| VERSION               | AX036741.1                        | GI:11226250   |                 |
| KEYWORDS              |                                   |   |                 |
| SOURCE                |                                   |   |                 |
| ORGANISM              |                                   |   |                 |
| REFERENCE             |                                   |   |                 |
| AUTHORS               |                                   |   |                 |
| TITLE                 |                                   |   |                 |
| JOURNAL               |                                   |   |                 |
| FEATURES              |                                   |   |                 |
| source                |                                   |   |                 |
| promoter              |                                   |   |                 |
| BASE COUNT            |                                   |   |                 |
| ORIGIN                |                                   |   |                 |
| Query Match           |                                   |   |                 |
| Best Local Similarity |                                   |   |                 |
| Matches 153:          |                                   |   |                 |
| QY                    | 78                                | CATGACACTCTGTGCGAATATTGAAGACGTAGACACTGACGACCAATGAAAGACAA    | 137             |
| DB                    | 63                                | CATGCACACTCTGTGCGAATATTGAAGACGTAGACACTGACGACCAATGAAAGACAA   | 122             |
| QY                    | 138                               | GATAAGTCGCGGATTGTGAAAGACACATATAGGACACATGTAAAGTCGAAATGTAAAG  | 197             |
| DB                    | 123                               | GATTAAGTCGCGGATTGTG-AAAGACATATAGGACACATGTAAAGTCGAAATGTAAAG  | 181             |
| QY                    | 198                               | GCGGAAGTAACCTTATGCATTGTGTAATTTGGTTAC                        | 233             |
| DB                    | 182                               | GCGGAAGTAACCTTATGCATTGTGTAATTTGGTTAC                        | 217             |
| RESULT 14             |                                   |   |                 |
| LOCUS                 | AX036740                          | 398 bp  | DNA             |
| DEFINITION            | Sequence 6 from Patent WO0058485. |   | Linear          |
| ACCESSION             | AX036740                          |   | PAT 16-NOV-2000 |
| VERSION               | AX036740.1                        | GI:11226249   |                 |
| KEYWORDS              |                                   |   |                 |
| SOURCE                |                                   |   |                 |
| ORGANISM              |                                   |   |                 |
| REFERENCE             |                                   |   |                 |
| AUTHORS               |                                   |   |                 |
| TITLE                 |                                   |   |                 |
| JOURNAL               |                                   |   |                 |
| FEATURES              |                                   |   |                 |
| source                |                                   |   |                 |





us-09-963-803-20.rng

True Apr 15 15:12:14 2003

Genome version 5.1.4  
 Copyright (c) 1993 - 2003  
 Genomic alignment time 149.237 Seconds  
 Alignment without alignments  
 61.612 Million cell updates/sec

OM nucleic - nucleic search using sw mode (without alignments)  
 Run on 05-09-963-803-20  
 1 seqs, 1125999159 residues  
 4370478

Title: April 14, 2003, 04:03:11  
 Sequence: 1 seqs, 1125999159 residues  
 Satisfying chosen parameters:

Score table:  
 0  
 2000000000  
 Minimum Match 08  
 Maximum Match 100%

Listing first 45 summaries  
 N.Geneseq.101002:\*

- 1: /SID52/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:\*
- 2: /SID52/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:\*
- 3: /SID52/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:\*
- 4: /SID52/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:\*
- 5: /SID52/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:\*
- 6: /SID52/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:\*
- 7: /SID52/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:\*
- 8: /SID52/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:\*
- 9: /SID52/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:\*
- 10: /SID52/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:\*
- 11: /SID52/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:\*
- 12: /SID52/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:\*
- 13: /SID52/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:\*
- 14: /SID52/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:\*
- 15: /SID52/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:\*
- 16: /SID52/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:\*
- 17: /SID52/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:\*
- 18: /SID52/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:\*
- 19: /SID52/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:\*
- 20: /SID52/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:\*
- 21: /SID52/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:\*
- 22: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001.DAT:\*
- 23: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:\*
- 24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2003.DAT:\*

pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed.  
 and is derived by analysis of the total score distribution.

| Result | No. | Score | Match | Length | ID      | Description         |
|--------|-----|-------|-------|--------|---------|---------------------|
| 1      | 462 | 100.0 | 462   | 21     | AA96854 | Nucleotide sequence |
| 2      | 374 | 80.7  | 541   | 21     | AA96855 | Nucleotide sequence |
| 3      | 354 | 76.0  | 541   | 21     | AA96856 | Nucleotide sequence |
| 4      | 262 | 52.0  | 541   | 21     | AA96857 | Nucleotide sequence |
| 5      | 240 | 46.0  | 541   | 21     | AA96858 | Nucleotide sequence |
| 6      | 212 | 43.4  | 541   | 21     | AA96859 | Nucleotide sequence |
| 7      | 200 | 43.4  | 541   | 21     | AA96860 | Nucleotide sequence |
| 8      | 200 | 43.4  | 541   | 21     | AA96861 | Nucleotide sequence |

|    |       |      |     |    |         |                     |
|----|-------|------|-----|----|---------|---------------------|
| 10 | 152.8 | 33.1 | 371 | 21 | AA96839 | Nucleotide sequence |
| 11 | 140.8 | 30.5 | 301 | 21 | AA96840 | Nucleotide sequence |
| 12 | 140.8 | 30.5 | 398 | 21 | AA96841 | Nucleotide sequence |
| 13 | 140.8 | 26.1 | 392 | 21 | AA96842 | Nucleotide sequence |
| 14 | 120.6 | 26.1 | 411 | 21 | AA96843 | Nucleotide sequence |
| 15 | 120.6 | 26.1 | 515 | 21 | AA96844 | Nucleotide sequence |
| 16 | 120.6 | 26.1 | 515 | 21 | AA96845 | Nucleotide sequence |
| 17 | 120.6 | 26.1 | 528 | 21 | AA96846 | Nucleotide sequence |
| 18 | 120.6 | 26.1 | 528 | 21 | AA96847 | Nucleotide sequence |
| 19 | 120.6 | 26.1 | 528 | 21 | AA96848 | Nucleotide sequence |
| 20 | 120.6 | 26.1 | 528 | 21 | AA96849 | Nucleotide sequence |
| 21 | 120.6 | 26.1 | 528 | 21 | AA96850 | Nucleotide sequence |
| 22 | 120.6 | 26.1 | 528 | 21 | AA96851 | Nucleotide sequence |
| 23 | 120.6 | 26.1 | 528 | 21 | AA96852 | Nucleotide sequence |
| 24 | 120.6 | 26.1 | 528 | 21 | AA96853 | Nucleotide sequence |
| 25 | 120.6 | 26.1 | 528 | 21 | AA96854 | Nucleotide sequence |
| 26 | 120.6 | 26.1 | 528 | 21 | AA96855 | Nucleotide sequence |
| 27 | 120.6 | 26.1 | 528 | 21 | AA96856 | Nucleotide sequence |
| 28 | 120.6 | 26.1 | 528 | 21 | AA96857 | Nucleotide sequence |
| 29 | 120.6 | 26.1 | 528 | 21 | AA96858 | Nucleotide sequence |
| 30 | 120.6 | 26.1 | 528 | 21 | AA96859 | Nucleotide sequence |
| 31 | 120.6 | 26.1 | 528 | 21 | AA96860 | Nucleotide sequence |
| 32 | 120.6 | 26.1 | 528 | 21 | AA96861 | Nucleotide sequence |
| 33 | 120.6 | 26.1 | 528 | 21 | AA96862 | Nucleotide sequence |
| 34 | 120.6 | 26.1 | 528 | 21 | AA96863 | Nucleotide sequence |
| 35 | 120.6 | 26.1 | 528 | 21 | AA96864 | Nucleotide sequence |
| 36 | 120.6 | 26.1 | 528 | 21 | AA96865 | Nucleotide sequence |
| 37 | 120.6 | 26.1 | 528 | 21 | AA96866 | Nucleotide sequence |
| 38 | 120.6 | 26.1 | 528 | 21 | AA96867 | Nucleotide sequence |
| 39 | 120.6 | 26.1 | 528 | 21 | AA96868 | Nucleotide sequence |
| 40 | 120.6 | 26.1 | 528 | 21 | AA96869 | Nucleotide sequence |
| 41 | 120.6 | 26.1 | 528 | 21 | AA96870 | Nucleotide sequence |
| 42 | 120.6 | 26.1 | 528 | 21 | AA96871 | Nucleotide sequence |
| 43 | 120.6 | 26.1 | 528 | 21 | AA96872 | Nucleotide sequence |
| 44 | 120.6 | 26.1 | 528 | 21 | AA96873 | Nucleotide sequence |
| 45 | 120.6 | 26.1 | 528 | 21 | AA96874 | Nucleotide sequence |

ALIGNMENTS

RESULT 1  
 AA96854 standard: DNA: 462 BP.  
 ID  
 AA96854: (first entry)  
 19-FEB-2001  
 Nucleotide sequence of chimeric expression promoter MFL163.  
 DE Promoter: intergenic region: Comelina yellow mottle virus.  
 KW Promoter: intergenic region: Plant vascular expression promoter: Cassava vein mosaic virus.  
 KW Plant green tissue chimera: ss.  
 KW Transgenic plant: chimera.  
 KW Chimeric - Comelina yellow mottle virus.  
 OS Chimeric - Cassava vein mosaic virus.  
 PN WO200058485-A1.  
 PD 05-OCT-2000.  
 XX 2000WO-IB00370.  
 XX 29-MAR-2000: 2000WO-0003925.  
 XX 29-MAR-1999: 99FR-0003925.  
 XX (MERI-) MERISTEM THERAPEUTICS.  
 XX Rance I, Gruber V, Thelsen M.  
 XX WPI: 2000-647238/62.

Tue Apr 15 15:12:14 2003

us-09-963-803-20.rng

Chimeric expression promoter for transgenic plant production, comprises sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region

Claim 5: Page 86; 91pp: English.

The present sequence represents a chimeric promoter of the invention. The specification describes a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter are derived from intergenic regions. The chimeric promoters are useful for producing transgenic plants.

Sequence 462 BP; 148 A; 87 C; 111 G; 116 T; 0 other:

Query Match 100.0%; Score 462; DB 21; Length 462;  
Best Local Similarity 100.0%; Pred. No. 1e-131; Indels 0; Gaps 0;  
Matches 462; Conservative 0; Mismatches 0;

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

Chimeric - Commelina yellow mottle virus.

Chimeric - Cassava vein mosaic virus.

WO200058485-A1.

05-OCT-2000.

29-MAR-2000; 2000MO-IB00370.

29-MAR-1999; 99FR-0003925.

(MERIT-) MERISTEM THERAPEUTICS.

Rance I, Gruber V, Thelsen M;

WPI: 2000-647238/62.

Chimeric expression promoter for transgenic plant production, comprises sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region

Claim 5: Page 86-87; 91pp: English.

The present sequence represents a chimeric promoter of the invention. The specification describes a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter are derived from intergenic regions. The chimeric promoters are useful for producing transgenic plants.

Sequence 600 BP; 188 A; 111 C; 147 G; 154 T; 0 other:

Query Match 80.9%; Score 373.6; DB 21; Length 600;  
Best Local Similarity 95.3%; Pred. No. 1.5e-104; Indels 0; Gaps 0;  
Matches 385; Conservative 0; Mismatches 19;

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60

1 AAGCTTCATGCTGCTGAGCAGTATCCGCTCATCATGATCATCATCATCTGA 60



Db 61 GGAGTGATAGCTAGCCACTGACACTCTGTGGCAATATTGAAAGCTAAGCATGACATGACGAC 120  
 |||||||  
 Qy 121 AACAAATGAAAAAGAAAGATTAAGTTCGGTATTTGAAAGACATAGAGACATGTA 180  
 |||||||  
 Db 121 AACAAATGAAAAAGAAAGATTAAGTTCGGTATTTGAAAGACATAGAGACATGTA 180  
 |||||||  
 Qy 181 ACGTGGAAAAATGTAAAGGGCGGAAAGTAACTTATGCAATTTGTAAATTGGTT 231  
 |||||||  
 Db 181 ACGTGGAAAAATGTAAAGGGCGGAAAGTAACTTATGCAATTTGTAAATTGGTT 231  
 |||||||  
 Qy 241 GATTGATGTCAATCAAGTTGATGTATCTCCACTGACGTAAAGGATGACGATGCC 300  
 |||||||  
 Db 241 GATTGATGTCAATCAAGTTGATGTATCTCCACTGACGTAAAGGATGACGATGCC 300  
 |||||||  
 Qy 232 ----- 231  
 |||||||  
 Db 301 ACGCACTAGTATGATGTGATATCAAGATTGATGATGTATCTCCACTGACGTAAAGGATG 291  
 |||||||  
 Qy 232 ACGCACTAGTATGATGTGATATCAAGATTGATGATGTATCTCCACTGACGTAAAGGATG 291  
 |||||||  
 Db 361 ACGCATGCCACGTTACCGGATATCCGGGTTCCCAAGCTTTATTTCCCTATTAAAGCACTT 420  
 |||||||  
 Qy 361 ACGCATGCCACGTTACCGGATATCCGGGTTCCCAAGCTTTATTTCCCTATTAAAGCACTT 420  
 |||||||  
 Db 292 ACGCATGCCACGTTACCGGATATCCGGGTTCCCAAGCTTTATTTCCCTATTAAAGCACTT 452  
 |||||||  
 Qy 421 GTGTACTAGCTTAAAAAACCAACACACACACACACTTGAAGGATCC 393  
 |||||||  
 Db 352 GTGTACTAGCTTAAAAAACCAACACACACACACACTTGAAGGATCC 393  
 |||||||

RESULT 5  
 AAA96857 standard; DNM: 604 BP.  
 ID AAA96857  
 XX  
 NC AAA96857;

(first entry)  
 (not a header entry)

peptide sequence of chimeric virus:  
 Intergenic region; Commelina yellow mottle virus;  
 expression promoter; plant vascular expression promoter;  
 green tissue expression promoter; Cassava vein mosaic virus  
 PR plant; chimera: ss.  
 XX commelina yellow mottle virus.  
 PA (Maava vein mosaic virus).  
 XX  
 PI  
 XX  
 DR  
 XX  
 XX  
 PT  
 PT  
 PT  
 PT  
 PS  
 Claim 5.

CC The present sequence represents a plant production, comprising  
CC the specific region replaced by a nucleic acid sequence, expressed  
CC from a first plant comprising a chimeric promoter region  
CC promoter region is replaced, in which a plant promoter comprising  
CC a second plant promoter comprising a plant green tissue expression

CC promoter region. Preferably, the first plant promoter originates from  
CC *Comelina* yellow mottle virus, and the second plant promoter are  
CC from the *Cassava* vein mosaic virus. Especially, the promoters are useful  
CC derived from intergenic plants. The climeric promoters are useful  
CC for producing transgenic plants.

xx Sequence 604 BP; 186 A; 116 C; 145 G; 157 T; 0 other;  
SQ

Query Match 56.7%; Score 262; DB 21; Length 604; Gaps  
Best Local Similarity 83.3%; 0; Mismatches 5; Indels 70; Caps  
Matches 375; Conservative

7A CATGACACTGTGCGAATTTGAGACGCTACGACTGCAGCAACATGANAAGAA 137  
TTTTCGACGACGAGCAACATGANAAGAA 219

[illegible]

|          |  |
|----------|--|
| RESULT 6 |  |
| AAA96855 | AAA96855 standard; DNA; 392 bp.                                    |
| ID       | AAA96855 standard; DNA; 392 bp.                                    |
| AA       | AAA96855 standard; DNA; 392 bp.                                    |
| AC       | AAA96855 standard; DNA; 392 bp.                                    |
| XX       | AAA96855 standard; DNA; 392 bp.                                    |
| XX       | AAA96855 standard; DNA; 392 bp.                                    |
| XX       | AAA96855 standard; DNA; 392 bp.                                    |
| DT       | 19-FEB-2001 (first entry)  |
| DE       | Nucleotide sequence of chimeric expression promoter MP1164.        |
| XX       | Nucleotide sequence of chimeric expression promoter MP1164.        |
| XX       | Nucleotide sequence of chimeric expression promoter MP1164.        |
| KW       | Promoter: intergenic region; Commelina yellow mottle virus;        |
| KW       | chimeric expression promoter; plant vascular expression promoter;  |
| KW       | plant green tissue expression promoter; Cassava vein mosaic virus. |
| KW       | transgenic plant; chimera; ss.                                     |
| XX       | transgenic plant; chimera; ss.                                     |
| XX       | transgenic plant; chimera; ss.                                     |
| OS       | Chimeric - Commelina yellow mottle virus.                          |
| OS       | Chimeric - Cassava vein mosaic virus.                              |
| XX       | Chimeric - Cassava vein mosaic virus.                              |
| PN       | WO200058485-A1.  |
| XX       | WO200058485-A1.  |
| PD       | 05-OCT-2000.   |
| XX       | 05-OCT-2000.   |
| PF       | 29-MAR-2000; 2000MO-IB00370.                                       |
| XX       | 29-MAR-2000; 2000MO-IB00370.                                       |
| PR       | 29-MAR-1999; 99FR-0003925.   |
| XX       | 29-MAR-1999; 99FR-0003925.   |
| PA       | (MERI-) MERISTEM THERAPEUTICS.                                     |
| XX       | (MERI-) MERISTEM THERAPEUTICS.                                     |



|   |   |
|---|---|
| Pt  | Rance I, Gruber V, Theisen M;   |
| Dx  | WPI: 2000-647238/62.  |
| Xx  |   |
| Pt  | Chimeric expression promoter for transgenic plant production, comprises |
| Pt  | sequence from promoter comprising vascular expression region replaced   |
| Pt  | with sequence from promoter comprising green tissue expression region   |
| Pt  | -   |
| Xx  |   |
| Ps  | Claim 5; Page 86; 91pp; English.  |
| Xx  |   |
| Cc  | The present sequence represents a chimeric promoter of the invention.   |
| Cc  | The specification describes chimeric expression promoters. These        |
| Cc  | chimeric promoters comprise a nucleic acid sequence which is derived    |
| Cc  | from a first plant promoter, in which a plant vascular expression       |
| Cc  | promoter region is replaced with a nucleic acid sequence derived from   |
| Cc  | a second plant promoter comprising a plant green tissue expression      |
| Cc  | promoter region. Preferably, the first plant promoter originates from   |
| Cc  | Commelina yellow mottle virus, and the second plant promoter originates |
| Cc  | from the Cassava vein mosaic virus. Especially, the promoters are       |
| Cc  | derived from intergenic regions. The chimeric promoters are useful      |
| Cc  | for producing transgenic plants.  |
| Xx  |   |
| S0  | Sequence 392 BP; 127 A; 80 C; 87 G; 98 T; 0 other;                      |
|   |   |
|   | Query Match            52.0%; Score 240.2; DB 21; Length 392;           |
|   | Best Local Similarity   77.4%; Pred. No. 1.le-63;                       |
|   | Matches 349; Conservative 0; Mismatches 33; Indels - 69; Gaps           |
|   |   |
| Qy  | 1 AACGTCGATCGCTCCAGCACCACATGATGCCGGTATCATATGACATCATCAAGTA               |
| Db  | 1 AAGCTGTATGCCTCCAGCACACTAGTATCCGGCTATCATATGACATCATCAAGTA               |
| Qy  | 61 GGAGTAGAATAGCTACGACATGACACTCTGTGGGAATTTGAAGAGCTAGACACTGACGC          |
| Db  | 61 GGAGTAGAATAGCTACGACATGACACTCTGTGGGAATTTGAAGAGCTAGACACTGACGC          |
| Qy  | 121 AACAAAGAAAAGAGAAGATAAGTGCGGTGATTGAAAAGACACATAGAGACACATGTA           |
| Db  | 121 AACAAAGAAAAGAGAAGATAAGTGCGGTGATTGAAAAGACACATAGAGACACATGTA           |
| Qy  | 181 AGGTGGAAGAAATGTAAGGGCGGAAAGTAACCTTATGCTATTTGGTTACGACTAGT            |
| Db  | 181 AGGTGGAAGAAATGTAAGGGCGGAAAGTAACCTTATGCTATTTGGTTACGACTAGT            |
| Qy  | 241 GATTGATGTGATATCAAGATTGATGTGATATCTCCAGTAGCTAAGGGATGACGATGCC          |
| Db  | 241 -----TGGCATTGGCTATCTCC-----TGGCATTGGCTATCTCC                        |
| Qy  | 301 ACGACTAGTGTATGATATCATCAAGATTGATGTGATATCTCCAGTAGCTAAGGGATG           |
| Db  | 251 TTACGTACGTGAGAGATATCATCAATCTTGTATATCACATC-----                      |
| Qy  | 361 ACCGATGCCACGTTAACCCGGTATGCCGGTTCCTCCAAGCTTATTTCTTATTTAAGCATT        |
| Db  | 292 AATCAGTATGATGATACCCGGTATGCCGGTTCCTCCAAGCTTATTTCTTATTTAAGCATT        |
| Qy  | 421 GTGTAGTACTTAGAAAAACAACAACAAC 451                                    |
| Db  | 352 GTGTAGTACTTAGAAAAACAACAACAAC 382                                    |
|   |   |
| RESULT 7  |   |
| ID AAA96837   |   |
| AAA96837 standard; DNA; 317 BP.                             |   |
| AAA96837:   |   |
| 19-FEB-2001 (first entry)                                   |   |
| Nucleotide sequence of chimeric expression promoter MP1116. |   |
| Promoter; intergenic region; Commelina yellow mottle virus; |   |

| Query Match  | Best Local Similarity                                       | Score              | DB     | Length |
|--|---|--------------------|--------|--------|
| Matches 213; Conservative 0; Mismatches 1; Indels 0; Gaps 0; | 46.0%;  | 212.4;             | DB 21; | 317;   |
|  | 99.5%;  | Pred. No. 3.4e-55; |        |        |
| Query 20   | ACTAGTATCCGCGGCATCATGACATCATCTATCAGACTAGGAGAGATGATAGTACGCA  | 79                 |        |        |
| Db 18  | ACTAGTATCCGCGGCATCATGACATCATCTATCAGACTAGGAGAGATGATAGTACGCA  | 77                 |        |        |
| Query 80   | TGACACTCTGTCGCAATATGTAAGACGTAGACGTAGACACAACATGAAAGAAAGA     | 139                |        |        |
| Db 78  | TGACACTCTGTCGCAATATGTAAGACGTAGACGTAGACACAACATGAAAGAAAGA     | 137                |        |        |
| Query 140  | TAAAGTCGGTATGTTGTAAGAGACATGAGACACATGTAAGTGTGAATAATGTAAGGC   | 199                |        |        |
| Db 138   | TAAAGTCGGTATGTTGTAAGAGACATGAGACACATGTAAGTGTGAATAATGTAAGGC   | 197                |        |        |
| Query 200  | GGAAGTAACCTTATGATCTTTGTAATTTGGTTAC                          | 233                |        |        |
| Db 198   | GGAAGTAACCTTATGATCTTTGTAATTTGGTTAC                          | 231                |        |        |
| Result 8   | AAA96859  |                    |        |        |
| ID   | AAA96859 standard; DNA; 472 BP.                             |                    |        |        |
| XX   | AAA96859;   |                    |        |        |
| XX   | 19-FEB-2001 (first entry)                                   |                    |        |        |
| XX   | Nucleotide sequence of chimeric expression promoter MP1169. |                    |        |        |

```
XX    19-FEB-2001   (first entry)
DT
DE      Nucleotide sequence of chimeric expression promoter MPr1117.
DX
XX
XX      Promoter; intergenic region; Commelina yellow mottle virus;
KW      chimeric expression promoter; plant vascular expression promoter;
KM      plant green tissue expression promoter; Cassava vein mosaic virus;
KK      transgenic plant; chimera; ss.
XX
OS      Chimeric - Commelina yellow mottle virus.
OS      Chimeric - Cassava vein mosaic virus.
PN      WO200058485-A1.
PD      05-OCT-2000.
PX
XX      29-MAR-2000; 2000WO-IB00370.
PY
XX      29-MAR-1999; 99FR-0003925.
PA      (MERIT-) MERISTEM THERAPEUTICS.
PI      Rance I, Gruber V, Theisen W;
PT      MPI; 2000-647238/62.
PS
CC      Claim 5; Page 81; 91pp; English.
CX
XX
CC      The present sequence represents a chimeric promoter of the invention.
CC      The specification describes chimeric expression promoters. These
CC      chimeric promoters comprise a nucleic acid sequence which is derived
CC      from a first plant promoter, in which a plant vascular expression
CC      promoter region is replaced with a nucleic acid sequence derived from
CC      a second plant promoter comprising a plant green tissue expression
CC      promoter region. Preferably, the first plant promoter originates from
CC      commelina yellow mottle virus, and the second plant promoter originates
CC      from the cassava vein mosaic virus. Especially, the promoters are
CC      derived from intergenic regions. The chimeric promoters are useful
CC      for producing transgenic plants.
CX
SQ      Sequence 348 BP; 116 A; 70 C; 78 G; 84 T; 0 other;
XX
Query Match          43.4%; Score 200.4; DB 21; Length 348;
Best local similarity 99.1%; Pred. No. 1,7e-51;
Matches 212; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY       20 ACTAGTATCGGCCGTCATCATGCACATCATTCAACACTGTGAAGAATGTAAGTTAAAGCCA 79
DB        |||||||
DB       52 ACTAGTATCGGCCGTCATCATGCACATCATTCAACACTGTGAAGAATGTAAGTTAAAGCCA 111
QY       80 TGACACTCTTGCGCAAATTTGAAGACGTAACCATACTGGACGACAACAATGAAAAGAAAGA 139
DB        |||||||
DB     112 TGACACTCTTGCGCAAATTTGAAGACGTAACCATACTGGACGACAACAATGAAAAGAAAGA 171
QY     140 TAAGTCGGTAGTATTGTGTAAGAACAGACATAGAGACACATGTAAAGTGAATAAATGTAAGGGC 199
DB        |||||||
DB     172 TAGGTTCGGTAGTATTGTG-TAAGACACATRAGAGACACATGTAAAGTGAATAAATGTAAGGGC 230
QY       200 GGAAAGTAACCTTATGCATTTTTGTAATTTGGTTAC 233
DB        |||||||
DB     231 GGAAGTAACCTTATGCATTTTGTAACTGTTAC 264
RESULT 10
ID AAA96839 standard; DNA; 371 bp.
```

|    |   |
|----|---|
| XX | Nucleotide sequence of chimeric expression promoter MP1154.             |
| DE |   |
| XX | Promoter; intergenic region; Commelina yellow mottle virus;             |
| KW | Chimeric expression promoter; plant vascular expression promoter;       |
| KW | plant green tissue expression promoter; Cassava vein mosaic virus;      |
| KW | transgenic plant; chimera; ss.  |
| XX |   |
| OS | Chimeric - Commelina yellow mottle virus.                               |
| OS | Chimeric - Cassava vein mosaic virus.                                   |
| XX |   |
| PN | WO200058485-A1.   |
| PD |   |
| PD | 05-OCT-2000.  |
| XX |   |
| PF | 29-MAR-2000; 2000WO-IB00370.  |
| XX |   |
| PR | 29-MAR-1999; 99FR-0003925.  |
| XX |   |
| PA | (MERI-) MERISTEM THERAPEUTICS.  |
| XX |   |
| PI | Rance I, Gruber V, Theisen M;   |
| XX |   |
| DR | WPI: 2000-647238/62.  |
| XX |   |
| PT | Chimeric expression promoter for transgenic plant production, comprises |
| PT | sequence from promoter comprising vascular expression region replaced   |
| PT | with sequence from promoter comprising green tissue expression region   |
| XX |   |
| PS | Claim 5; Page 82; 91pp; English.  |
| XX |   |
| CC | The present sequence represents a chimeric promoter of the invention.   |
| CC | The specification describes chimeric expression promoters. These        |
| CC | chimeric promoters comprise a nucleic acid sequence which is derived    |
| CC | from a first plant promoter, in which a plant vascular expression       |
| CC | promoter region is replaced with a nucleic acid sequence derived from   |
| CC | a second plant promoter comprising a plant green tissue expression      |
| CC | promoter region. Preferably, the first plant promoter originates from   |
| CC | Commelina yellow mottle virus, and the second plant promoter originates |
| CC | from the Cassava vein mosaic virus. Especially, the promoters are       |
| CC | derived from intergenic regions. The chimeric promoters are useful      |
| CC | for producing transgenic plants.  |
| XX |   |
| SO | Sequence 301 BP; 98 A; 54 C; 74 G; 75 T; 0 other;                       |
|    |   |
|    | Query Match 30.5%; Score 140.8; DB 21; Length 301;                      |
|    | Best Local Similarity 98.1%; Pred. No. 3.1e-33;                         |
|    | Mismatch 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;           |
| QY | 78 CATGCACTGCTGGGATATTGAAGAGTAAGCACTGACGACACAACTGAAAAGAGA 137           |
| DB | 63 CATGCCACTGCTGGGATATTGAAGAGTAAGCACTGACGACAACTGAAAAGAGA 122            |
| QY | 138 GATAAGTCGGTGTATTGGAAGAGACATAGAGACACATGTAAAGTGAATTAAG 197            |
| DB | 123 GATAAGTCGGTGTATTGGAAGAGACATAGAGACACATGTAAAGTGAATTAAG 181            |
| QY | 198 GCGGAAGTAACCTTATGCATTTGTAATTTGGTTAC 233                             |
| DB | 182 GCGGAAGTAACCTTATGCATTTGTAATTTGGTTAC 217                             |
|    |   |
|    | RESULT 12   |
|    | AAA96840  |
|    | ID AAA96840 standard; DNA; 398 BP.                                      |
|    | AAA96840;   |
|    | AC  |
|    | XX  |
|    | XX  |
|    | 19-FEB-2001 (first entry)   |
|    | DT  |
|    | XX  |
|    | XX  |
|    | Nucleotide sequence of chimeric expression promoter MP1147.             |

KM Promoter: intergenic region; Commelina yellow mottle virus;  
KM chimeric expression promoter; plant vascular expression promoter;  
KM plant green tissue expression promoter; Cassava vein mosaic virus;  
KM transgenic plant; chimera; ss.  
XX  
OS Chimeric - Commelina yellow mottle virus.  
OS Chimeric - Cassava vein mosaic virus.  
XX  
PN WO200058485-A1.  
XX  
PD 05-OCT-2000.  
XX  
PF 29-MAR-2000; 2000WO-IB00370.  
XX  
PR 29-MAR-1999; 99PR-0003925.  
XX  
PA (MERI-) MERISTEM THERAPEUTICS.  
XX  
PI Rance I, Gruber V, Theisen M;  
XX  
DR WPI; 2000-647238/62.  
XX  
PT Chimeric expression promoter for transgenic plant production, comprises  
PT sequence from promoter comprising vascular expression region replaced  
PT with sequence from promoter comprising green tissue expression region  
PT  
XX  
PS Claim 5; Page 82; 91pp; English.  
XX  
CC The present sequence represents a chimeric promoter of the invention.  
CC The specification describes chimeric expression promoters. These  
CC chimeric promoters comprise a nucleic acid sequence which is derived  
CC from a first plant promoter, in which a plant vascular expression  
CC promoter region is replaced with a nucleic acid sequence derived from  
CC a second plant promoter comprising a plant green tissue expression  
CC promoter region. Preferably, the first plant promoter originates from  
CC Commelina yellow mottle virus, and the second plant promoter originates  
CC from the Cassava vein mosaic virus. Especially, the promoters are  
CC derived from intergenic regions. The chimeric promoters are useful  
CC for producing transgenic plants.  
XX  
SO Sequence 398 BP; 128 A; 80 C; 93 G; 97 T; 0 other;  
XX  
Query Match 30.5%; Score 140.8; DB 21; Length 398;  
Best Local Similarity 98.1%; Pred. No. 3.5e-33;  
Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
XX  
QY 78 CATGACACTGTGGCAATTGTAAGACCTAAGCAGTACGAGACACATATAAAGAAGAA 137  
DB 160 CATGCCACTGTGGCAATTGTAAGACGTAACGACTGACGACAAATGAAAAAGAGAA 219  
QY 138 GATAAGTCGCGTATTTGTAAGAGACATAGAGACATGTAAGTGAATGTAAGG 197  
DB 220 GATAAGTCGCGTATTTGTAAGAGACATAGAGACATGTAAGTGAATGTAAGG 278  
QY 198 GCGGAAAGTAACCTTATGCAATTTGTAATTTGGTTAC 233  
DB 279 GCGGAAAGTAACCTTATGCAATTTGTAATTTGGTTAC 314  
XX  
RESULT 13  
AAV14019  
ID AAV14019 standard; DNA; 392 BP.  
XX  
AC AAV14019;  
XX  
DT 18-JUN-1998 (first entry)  
XX  
DE CSMVW promoter CVP1.  
XX  
KM Cassava vein mosaic virus; CSMVW; promoter; cultivated crop;  
KM tissue-specific expression control; transgenic plant; ss.  
XX

OS Cassava vein mosaic virus.  
XX  
PN WO9748819-A1.  
XX  
PD 24-DEC-1997.  
XX  
PF 20-JUN-1997; 97WO-US10376.  
XX  
PR 20-JUN-1996; 96US-0020129.  
XX  
PA (SCRI) SCRIPPS RES INST.  
XX  
PI Beachy RN, De Kochko A, Fauquet C, Verdaguer B;  
XX  
DR WPI; 1998-063157/06.  
XX  
PT Cassava vein mosaic virus promoter - used to express heterologous  
PT DNA sequences for producing transgenic plants having altered  
PT phenotype(s)  
XX  
PS Claim 2; Page 74; 115pp; English.  
XX  
CC This sequence represents a cassava vein mosaic virus promoter, and  
CC is a nucleic acid molecule of the invention. The promoter is capable of  
CC initiating transcription of an operably linked heterologous nucleic acid  
CC sequence in a plant cell. The CSMVW promoters are active in both monocot  
CC and dicot plant species, and therefore can be readily applied to a  
CC variety of cultivated crops. Although generally constitutive, the  
CC derivative promoters include promoters that can regulate expression in a  
CC tissue-specific manner, and therefore are useful for controlling  
CC expression of heterologous genes in a tissue-specific manner. The  
CC promoters can be used for producing transgenic plants with an altered  
CC phenotype.  
XX  
SO Sequence 392 BP; 154 A; 64 C; 83 G; 91 T; 0 other;  
XX  
Query Match 26.1%; Score 120.6; DB 19; Length 392;  
Best Local Similarity 93.3%; Pred. No. 5.5e-27;  
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
XX  
QY 93 GAATTTGAAGACGTAAAGCCTGACGACCAACATGAAGAAAGACATTAAGTCGGTGA 152  
DB 143 GAATCTTGAAGACGTAAAGCCTGACGACCAACATGAAGAAAGACATTAAGTCGGTGA 202  
QY 153 TGTGAAGACATAGAGACATGTAAGTGAAGTGAAGGCGGAAAGTAACCTT 212  
DB 203 TGTGAAGACATAGAGACATGTAAGTGAAGTGAAGGCGGAAAGTAACCTT 262  
QY 213 ATGCATTTGTAATTT 227  
DB 263 ATCAACAAGCAATCT 277  
XX  
RESULT 14  
AAV14021  
ID AAV14021 standard; DNA; 411 BP.  
XX  
AC AAV14021;  
XX  
DT 18-JUN-1998 (first entry)  
XX  
DE CSMVW promoter PB.  
XX  
KM Cassava vein mosaic virus; CSMVW; promoter; cultivated crop;  
KM tissue-specific expression control; transgenic plant; ss.  
XX  
OS Cassava vein mosaic virus.  
XX  
PN WO9748819-A1.  
XX  
PD 24-DEC-1997.  
XX  
PF 20-JUN-1997; 97WO-US10376.  
XX

```
XX 20-JUN-1996; 96US-0020129.
PR (SCRI ) SCRIPPS RES INST.
PA Beachy RN, De Kochko A, Fauquet C, Verdagner B;
XX WPI; 1998-063157/06.
DR
XX
XX Cassava vein mosaic virus promoter - used to express heterologous
PT DNA sequences for producing transgenic plants having altered
PT phenotype(s)
XX
XX Claim 2; Page 76-77; 115pp; English.
XX
CC This sequence represents a cassava vein mosaic virus promoter, and
CC is a nucleic acid molecule of the invention. The promoter is capable of
CC initiating transcription of an operably linked heterologous nucleic acid
CC sequence in a plant cell. The CaMV promoters are active in both monocot
CC and dicot plant species, and therefore can be readily applied to a
CC variety of cultivated crops. Although generally constitutive, the
CC derivative promoters include promoters that can regulate expression in a
CC tissue-specific manner, and therefore are useful for controlling
CC expression of heterologous genes in a tissue-specific manner. The
CC promoters can be used for producing transgenic plants with an altered
CC phenotype.
XX
SQ Sequence 411 BP; 157 A; 60 C; 87 G; 107 T; 0 other;

Query Match 26.1%; Score 120.6; DB 19; Length 411;
Best Local Similarity 93.3%; Pred. No. 5.6e-27;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 93 GAATATTGAAGACCTAGCACTGACGACACATGAAAGAAAGATAGGTGGTGAT 152
DB 107 GAACTCTGAAGACCTAGCACTGACGACACATGAAAGAAAGATAGGTGGTGAT 166
QY 153 TGTGAAGAGACATAGAGACACATGTAAGTGGAAATGTAAGCGGGAATACCTT 212
DB 167 TGTGAAGAGACATAGAGACACATGTAAGTGGAAATGTAAGCGGGAATACCTT 226
QY 213 ATGCATTTGTAATTT 227
DB 227 ATCACAAGGAATCT 241

RESULT 15
AAA96836
ID AAA96836 standard; DNA; 515 BP.
XX
XX AAA96836;
AC
XX
DT 19-FEB-2001 (first entry)
XX
DE Promoter from intergenic region of Cassava vein mosaic virus.
XX
KM Promoter: intergenic region; Commelina yellow mottle virus;
KW chimeric expression promoter; plant vascular expression promoter;
KW plant green tissue expression promoter; Cassava vein mosaic virus;
transgenic plant; ss.
XX
XX Cassava vein mosaic virus.
OS
XX
PN MO200058485-A1.
XX
PD 05-OCT-2000.
XX
PF 29-MAR-2000; 2000MO-IB00370.
XX
PR 29-MAR-1999; 99FR-0003925.
XX
PA (MERI-) MERISTEM THERAPEUTICS.
```

```
PI Rance I, Gruber V, Thelsen M;
XX
XX WPI; 2000-647238/62.
DR
XX
XX Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
XX
XX Claim 4; Page 80; 91pp; English.
XX
XX
CC The present sequence represents a promoter fragment from the intergenic
CC region of Cassava vein mosaic virus. The promoter is used to construct
CC chimeric expression promoters. These chimeric promoters comprise a
CC nucleic acid sequence which is derived from a first plant promoter,
CC in which a plant vascular expression promoter region is replaced with
CC a nucleic acid sequence derived from a second plant promoter comprising
CC a plant green tissue expression promoter region. Preferably, the first
CC plant promoter originates from Commelina yellow mottle virus, and the
CC second plant promoter originates from the Cassava vein mosaic virus.
CC The chimeric promoters are useful for producing transgenic plants.
XX
XX
SQ Sequence 515 BP; 198 A; 79 C; 109 G; 129 T; 0 other;

Query Match 26.1%; Score 120.6; DB 21; Length 515;
Best Local Similarity 93.3%; Pred. No. 6.1e-27;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 93 GAATATTGAAGACCTAGCACTGACGACACATGAAAGAAAGATAGGTGGTGAT 152
DB 216 GAACTCTGAAGACCTAGCACTGACGACACATGAAAGAAAGATAGGTGGTGAT 275
QY 153 TGTGAAGAGACATAGAGACACATGTAAGTGGAAATGTAAGCGGGAATACCTT 212
DB 276 TGTGAAGAGACATAGAGACACATGTAAGTGGAAATGTAAGCGGGAATACCTT 335
QY 213 ATGCATTTGTAATTT 227
DB 336 ATCACAAGGAATCT 350
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Search completed: April 14, 2003, 08:19:38  
Job time : 151.237 secs



GenCore version 5.1.4.p5\_4578  
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## OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 08:01:47 ; Search time 47.6289 Seconds  
(without alignments)  
2974.765 Million cell updates/sec

Title: US-09-963-803-20

Perfect score: 462

Sequence: 1 aagcttcacgcctgcagca.....cacacacactagagatcc 462

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Issued\_Patents\_NA:\*

- 1: /cgn2\_6/ptodata/1/lna/5A.COMB.seq:\*
- 2: /cgn2\_6/ptodata/1/lna/5B.COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/lna/6A.COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/lna/6B.COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/lna/PCrUS.COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/lna/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 48.6  | 10.5        | 7218   | 1  | Sequence 14, Appli |
| 2          | 40.4  | 8.7         | 439    | 1  | Sequence 3, Appli  |
| 3          | 40.4  | 8.7         | 439    | 2  | Sequence 3, Appli  |
| 4          | 40.4  | 8.7         | 446    | 1  | Sequence 23, Appli |
| 5          | 40.4  | 8.7         | 532    | 3  | Sequence 1, Appli  |
| 6          | 40.4  | 8.7         | 532    | 4  | Sequence 1, Appli  |
| 7          | 40.4  | 8.7         | 532    | 4  | Sequence 1, Appli  |
| 8          | 40.4  | 8.7         | 532    | 4  | Sequence 1, Appli  |
| 9          | 40.4  | 8.7         | 532    | 4  | Sequence 1, Appli  |
| 10         | 40.4  | 8.7         | 532    | 4  | Sequence 1, Appli  |
| 11         | 40.4  | 8.7         | 532    | 4  | Sequence 1, Appli  |
| 12         | 40.4  | 8.7         | 532    | 4  | Sequence 1, Appli  |
| 13         | 40.4  | 8.7         | 560    | 3  | Sequence 5, Appli  |
| 14         | 40.4  | 8.7         | 560    | 4  | Sequence 5, Appli  |
| 15         | 40.4  | 8.7         | 560    | 4  | Sequence 5, Appli  |
| 16         | 40.4  | 8.7         | 560    | 4  | Sequence 5, Appli  |
| 17         | 40.4  | 8.7         | 560    | 4  | Sequence 5, Appli  |
| 18         | 40.4  | 8.7         | 560    | 4  | Sequence 5, Appli  |
| 19         | 40.4  | 8.7         | 560    | 4  | Sequence 5, Appli  |
| 20         | 40.4  | 8.7         | 560    | 4  | Sequence 5, Appli  |
| 21         | 40.4  | 8.7         | 661    | 4  | Sequence 33, Appli |
| 22         | 40.4  | 8.7         | 793    | 4  | Sequence 1, Appli  |
| 23         | 40.4  | 8.7         | 793    | 4  | Sequence 1, Appli  |
| 24         | 40.4  | 8.7         | 831    | 1  | Sequence 5, Appli  |
| 25         | 40.4  | 8.7         | 950    | 6  | Patent No. 5177308 |
| 26         | 40.4  | 8.7         | 978    | 1  | Sequence 31, Appli |
| 27         | 40.4  | 8.7         | 978    | 1  | Sequence 31, Appli |

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|----|------|-----|------|---|-------------------|--------------------|
| 28 | 40.4 | 8.7 | 979  | 1 | US-08-446-486-30  | Sequence 30, Appli |
| 29 | 40.4 | 8.7 | 979  | 1 | US-08-463-308-30  | Sequence 30, Appli |
| 30 | 40.4 | 8.7 | 980  | 6 | 525479-30         | Patent No. 5254799 |
| 31 | 40.4 | 8.7 | 1030 | 1 | US-07-936-163-46  | Sequence 46, Appli |
| 32 | 40.4 | 8.7 | 1030 | 4 | US-08-729-601A-43 | Sequence 43, Appli |
| 33 | 40.4 | 8.7 | 1034 | 4 | US-09-363-970-35  | Sequence 35, Appli |
| 34 | 40.4 | 8.7 | 1138 | 4 | US-09-011-151-8   | Sequence 8, Appli  |
| 35 | 40.4 | 8.7 | 1138 | 4 | US-09-011-151-9   | Sequence 9, Appli  |
| 36 | 40.4 | 8.7 | 1196 | 4 | US-08-729-601A-46 | Sequence 46, Appli |
| 37 | 40.4 | 8.7 | 1279 | 4 | US-09-185-244-2   | Sequence 2, Appli  |
| 38 | 40.4 | 8.7 | 1279 | 4 | US-09-471-913-6   | Sequence 6, Appli  |
| 39 | 40.4 | 8.7 | 1303 | 3 | US-08-894-440-2   | Sequence 2, Appli  |
| 40 | 40.4 | 8.7 | 1303 | 4 | US-09-458-093-2   | Sequence 2, Appli  |
| 41 | 40.4 | 8.7 | 1651 | 3 | US-09-065-999-5   | Sequence 5, Appli  |
| 42 | 40.4 | 8.7 | 1651 | 3 | US-09-065-999-6   | Sequence 6, Appli  |
| 43 | 40.4 | 8.7 | 1722 | 1 | US-08-247-809A-5  | Sequence 5, Appli  |
| 44 | 40.4 | 8.7 | 1722 | 2 | US-08-711-728-5   | Sequence 5, Appli  |
| 45 | 40.4 | 8.7 | 1829 | 1 | US-07-966-187-17  | Sequence 17, Appli |

## ALIGNMENTS

RESULT 1  
US-08-232-463-14/c  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHIEFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOXLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232.463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935.313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pT9gpc-F1s  
US-08-232-463-14  
Query Match 10.5% Score 48.6; DB 1; Length 7218;

Best Local Similarity 5.38; Pred. No. 2.7e-05;  
Matches 18; Conservative 185; Mismatches 134; Indels 0; Gaps 0;  
OY 59 GAGAGATGATAGCTGACCTGACACTCTGTGGCAATATTGAAGACGTAGCAGC 118  
DB 1367 RRR 1308  
OY 119 ACAACAATGAAAGAGAGATAAGTCGGTGAATTGTGAAGACATAGAGACATG 178  
DB 1307 RRR 1248  
OY 179 TAAGTGAATAATGTAAGCGCGAAGTAACTTATGATTTGTTAATGTTACGACTA 238  
DB 1247 RRR 1188  
OY 239 GTGATGATGATGATATCAAGATTGATGATATCTCCACTGACGTAGGATGACGATG 298  
DB 1187 RRR 1128  
OY 299 CCAGACTAGTGAATTGATGATATCAAGATTGATGATGATGATGATGATGATGATG 358  
DB 1127 RRR 1068  
OY 359 TGACGATGCCAGCTTACCGCGTATGCCGTTCCCA 395  
DB 1067 RATGCAAGCTCCCTGCAGCTGACCAAGCTCGAA 1031  
RESULT 2  
US-08-247-809A-3  
; Sequence 3, Application US/08247809A  
; Patent No. 5569823  
; GENERAL INFORMATION:  
; APPLICANT: Peter H. Schreier; Klaus Stenzel; Gunter Adam;  
; APPLICANT: Edgar Maiss  
; TITLE OF INVENTION: DEOXYRIBONUCLEIC ACIDS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS  
; STREET: 660 White Plains Road  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10591-5144  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB  
; MEDIUM TYPE: storage  
; COMPUTER: NEC Powermate 1 Plus  
; OPERATING SYSTEM: DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/247,809A  
; FILING DATE: May 23, 1994  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: P 43 178 45.6 (Germany)  
; FILING DATE: May 28, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kurt G. Briscoe  
; REGISTRATION NUMBER: 33,141  
; REFERENCE/DOCKET NUMBER: Bayer 9049-KGB.  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (914) 332-1700  
; TELEFAX: (914) 332-1844  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 439 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-247-809A-3

Query Match 8.7%; Score 40.4; DB 1: Length 439;  
Best Local Similarity 88.0%; Pred. No. 0.0028;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
OY 258 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCACGACTA 307  
DB 338 GATTGATGATATCTCCACTGACGTAAAGGATGACGACCAATCCGACTA 387  
RESULT 3  
US-08-711-728-3  
; Sequence 3, Application US/08711728  
; Patent No. 5973135  
; GENERAL INFORMATION:  
; APPLICANT: Peter H. Schreier; Klaus Stenzel; Gunter Adam;  
; APPLICANT: Edgar Maiss  
; TITLE OF INVENTION: DEOXYRIBONUCLEIC ACIDS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS  
; STREET: 660 White Plains Road  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10591-5144  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB  
; MEDIUM TYPE: storage  
; COMPUTER: NEC Powermate 1 Plus  
; OPERATING SYSTEM: DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/711,728  
; FILING DATE: 03-SEPT-1996  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/247,809  
; FILING DATE: 23-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 43178456  
; FILING DATE: 28-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kurt G. Briscoe  
; REGISTRATION NUMBER: 33,141  
; REFERENCE/DOCKET NUMBER: Bayer 9049.1-KGB  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (914) 332-1700  
; TELEFAX: (914) 332-1844  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 439 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-711-728-3  
Query Match 8.7%; Score 40.4; DB 2: Length 439;  
Best Local Similarity 88.0%; Pred. No. 0.0028;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
OY 258 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCACGACTA 307  
DB 338 GATTGATGATATCTCCACTGACGTAAAGGATGACGACCAATCCGACTA 387  
RESULT 4  
US-08-764-100-23  
; Sequence 23, Application US/08764100  
; Patent No. 5773700  
; GENERAL INFORMATION:



```

: APPLICANT: van Gilsven J., Martinus O.
: APPLICANT: De Haan, Petrus T.
: APPLICANT: Giejen L., Johannes J.
: APPLICANT: Peters, Dirk
: APPLICANT: Goldbach, Robert W.
: TITLE OF INVENTION: Improvements in or Relating to Organic
: NUMBER OF INVENTION: Compounds
: NUMBER OF SEQUENCES: 27
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sandoz Agro, Inc
: STREET: 975 California Avenue
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/764,100
: FILING DATE: 06-DEC-1996
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/214,064
: FILING DATE:
: APPLICATION NUMBER: US 08/032,235
: FILING DATE: 17-MAR-1993
: APPLICATION NUMBER: GB 9206016.9
: FILING DATE: 19-MAR-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: NO. 5773700rls, Allen E.
: REGISTRATION NUMBER: 34,490
: REFERENCE/DOCKET NUMBER: 137-1061
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 354-3592
: TELEFAX: (415) 857-1125
: INFORMATION FOR SEQ ID NO: 23:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 446 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-08-764-100-23
:
: Query Match      8.7%; Score 40.4; DB 1; Length 446;
: Best Local Similarity 88.0%; Pred. No. 0.0028;
: Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
:
OY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACCATGCCACGACTA 307
Db 274 GATTGATGTGATATCTCCACTGACGTAAAGGATGACCATGCCACACTA 323
:
: RESULT 5
: US-09-042-426-1
: Sequence 1, Application US/09042426
: Patent No. 6114608
: GENERAL INFORMATION:
: APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
: TITLE OF INVENTION: DNA Construct Containing Bacillus
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: NO. 6114608artlis Corporation
: STREET: 564 Morris Avenue
: CITY: Summit
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07901
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/291,238
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/042,426
: FILING DATE: March 13, 1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Hoxie, Thomas
: REGISTRATION NUMBER: 32,993
: REFERENCE/DOCKET NUMBER: 135/1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 541-8614
: TELEFAX: (919) 541-8689
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 532 base pairs
: TYPE: nucleic acid
```

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: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/042,426
: FILING DATE: March 13, 1998
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Hoxie, Thomas
: REGISTRATION NUMBER: 32,993
: REFERENCE/DOCKET NUMBER: 135/1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 541-8614
: TELEFAX: (919) 541-8689
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 532 base pairs
: TYPE: nucleic acid
:
: US-09-042-426-1
:
: Query Match      8.7%; Score 40.4; DB 3; Length 532;
: Best Local Similarity 88.0%; Pred. No. 0.003;
: Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
:
OY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACCATGCCACGACTA 307
Db 274 GATTGATGTGATATCTCCACTGACGTAAAGGATGACCATGCCACACTA 323
:
: RESULT 6
: US-09-291-238-1
: Sequence 1, Application US/09291238
: Patent No. 622104
: GENERAL INFORMATION:
: APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
: TITLE OF INVENTION: DNA Construct Containing Bacillus
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: NO. 622104artlis Corporation
: STREET: 564 Morris Avenue
: CITY: Summit
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07901
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/291,238
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/042,426
: FILING DATE: March 13, 1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Hoxie, Thomas
: REGISTRATION NUMBER: 32,993
: REFERENCE/DOCKET NUMBER: 135/1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 541-8614
: TELEFAX: (919) 541-8689
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 532 base pairs
: TYPE: nucleic acid
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STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: 35S Promoter  
US-09-291-238-1

Query Match 8.7% Score 40.4; DB 4; Length 532;  
Best Local Similarity 88.0%; Pred. No. 0.003;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCAGACTA 307  
|||||  
DB 274 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGACCAATCCACTA 323

## RESULT 7

US-09-330-760-1  
Sequence 1, Application US/09330760  
Patent No. 6229075

## GENERAL INFORMATION:

APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Stinbald  
TITLE OF INVENTION: DNA Construct Containing Bacillus  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6229075artis Corporation  
STREET: 564 Morris Avenue  
CITY: Summit  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07901

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/330,760  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/042,426  
FILING DATE: March 13, 1998  
ATTORNEY/AGENT INFORMATION:

NAME: Hoxie, Thomas

REGISTRATION NUMBER: 32,993

REFERENCE/DOCKET NUMBER: 135/1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 541-8614

TELEFAX: (919) 541-8689

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 532 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

IMMEDIATE SOURCE:

CLONE: 35S Promoter

US-09-330-760-1

Query Match 8.7% Score 40.4; DB 4; Length 532;

Best Local Similarity 88.0%; Pred. No. 0.003;

Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCAGACTA 307  
|||||  
DB 274 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGACCAATCCACTA 323

RESULT 8  
US-09-328-473-1  
Sequence 1, Application US/09328473  
Patent No. 6232533

## GENERAL INFORMATION:

APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Stinbald  
TITLE OF INVENTION: DNA Construct Containing Bacillus  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6232533artis Corporation  
STREET: 564 Morris Avenue  
CITY: Summit  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07901

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/328,473  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/042,426

FILING DATE: March 13, 1998

ATTORNEY/AGENT INFORMATION:

NAME: Hoxie, Thomas

REGISTRATION NUMBER: 32,993

REFERENCE/DOCKET NUMBER: 135/1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 541-8614

TELEFAX: (919) 541-8689

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 532 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

IMMEDIATE SOURCE:

CLONE: 35S Promoter

US-09-328-473-1

Query Match 8.7% Score 40.4; DB 4; Length 532;

Best Local Similarity 88.0%; Pred. No. 0.003;

Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCAGACTA 307  
|||||  
DB 274 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGACCAATCCACTA 323

## RESULT 9

US-09-330-737-1  
Sequence 1, Application US/09330737  
Patent No. 6232534

## GENERAL INFORMATION:

APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Stinbald  
TITLE OF INVENTION: DNA Construct Containing Bacillus  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6232534artis Corporation  
STREET: 564 Morris Avenue  
CITY: Summit  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07901

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/330,737  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,426  
FILING DATE: March 13, 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoxie, Thomas  
REGISTRATION NUMBER: 32,993  
REFERENCE/DOCKET NUMBER: 135/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8614  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 532 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: 35S Promoter  
US-09-330-737-1

Query Match  
Best Local Similarity 8.7%; Score 40.4; DB 4; Length 532;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 258 GATTGATGTCATCTCCACTGACGTAAAGGATGACCATGCCACACTA 307  
DB 274 GATTGATGTCATCTCCACTGACGTAAAGGATGACCATGCCACACTA 323

RESULT 10  
US-09-329-169-1  
Sequence 1, Application US/09329169  
Patent No. 6329575  
GENERAL INFORMATION:  
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi  
TITLE OF INVENTION: DNA Construct Containing Bacillus  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6329575artis Corporation  
STREET: 564 Morris Avenue  
CITY: Summit  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07901  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/329,169  
FILING DATE: 09-Jun-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/042,426  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoxie, Thomas  
REGISTRATION NUMBER: 32,993  
REFERENCE/DOCKET NUMBER: 135/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8614

TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 532 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: 35S Promoter  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-329-169-1

Query Match  
Best Local Similarity 8.7%; Score 40.4; DB 4; Length 532;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 258 GATTGATGTCATCTCCACTGACGTAAAGGATGACCATGCCACACTA 307  
DB 274 GATTGATGTCATCTCCACTGACGTAAAGGATGACCATGCCACACTA 323

RESULT 11  
US-09-330-714A-1  
Sequence 1, Application US/09330714A  
Patent No. 6342660  
GENERAL INFORMATION:  
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi  
TITLE OF INVENTION: DNA Construct Containing Bacillus  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6342660artis Corporation  
STREET: 564 Morris Avenue  
CITY: Summit  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07901  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/330,714A  
FILING DATE: 11-Jun-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/042,426  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoxie, Thomas  
REGISTRATION NUMBER: 32,993  
REFERENCE/DOCKET NUMBER: 135/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8614  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 532 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: 35S Promoter  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-330-714A-1

Query Match 8.7%; Score 40.4; DB 4; Length 532;  
Best Local Similarity 88.0%; Pred. No. 0.003;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 258 GATTGATGTGATATCTCCAGCTAGAGGATGACGATGCCAGCTA 307  
|||||  
Db 274 GATTGATGTGATATCTCCAGCTAGAGGATGACGATGCCAGCTA 323  
|||||

RESULT 12  
US-09-328-826-1  
; Sequence 1, Application US/09328826  
; Patent No. 6399860  
; GENERAL INFORMATION:  
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi  
; TITLE OF INVENTION: DNA Construct Containing Bacillus  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: No. 6399860artis Corporation  
; STREET: 564 Morris Avenue  
; CITY: Summit  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07901  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/328,826  
; FILING DATE: 09-Jun-1999  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/042,426  
; FILING DATE: March 13, 1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoxie, Thomas  
; REGISTRATION NUMBER: 32,993  
; REFERENCE/DOCKET NUMBER: 135/1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919) 541-8614  
; TELEFAX: (919) 541-8689  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 532 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; IMMEDIATE SOURCE:  
; CLONE: 35S Promoter  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-328-826-1

Query Match 8.7%; Score 40.4; DB 4; Length 532;  
Best Local Similarity 88.0%; Pred. No. 0.003;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 258 GATTGATGTGATATCTCCAGCTAGAGGATGACGATGCCAGCTA 307  
|||||  
Db 274 GATTGATGTGATATCTCCAGCTAGAGGATGACGATGCCAGCTA 323  
|||||

RESULT 13  
US-09-042-426-5  
; Sequence 5, Application US/09042426  
; Patent No. 6114608  
; GENERAL INFORMATION:  
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi  
; TITLE OF INVENTION: DNA Construct Containing Bacillus

NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: No. 6114608artis Corporation  
; STREET: 564 Morris Avenue  
; CITY: Summit  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07901  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/042,426  
; FILING DATE: March 13, 1998  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoxie, Thomas  
; REGISTRATION NUMBER: 32,993  
; REFERENCE/DOCKET NUMBER: 135/1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919) 541-8614  
; TELEFAX: (919) 541-8689  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 560 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; IMMEDIATE SOURCE:  
; CLONE: 35S Promoter  
US-09-042-426-5

Query Match 8.7%; Score 40.4; DB 3; Length 560;  
Best Local Similarity 88.0%; Pred. No. 0.0031;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 258 GATTGATGTGATATCTCCAGCTAGAGGATGACGATGCCAGCTA 307  
|||||  
Db 322 GATTGATGTGATATCTCCAGCTAGAGGATGACGATGCCAGCTA 371  
|||||

RESULT 14  
US-09-291-238-5  
; Sequence 5, Application US/09291238  
; Patent No. 6222104  
; GENERAL INFORMATION:  
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi  
; TITLE OF INVENTION: DNA Construct Containing Bacillus  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: No. 6222104artis Corporation  
; STREET: 564 Morris Avenue  
; CITY: Summit  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07901  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/291,238  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/042,426  
; FILING DATE: March 13, 1998

ATTORNEY/AGENT INFORMATION:  
NAME: Hoxie, Thomas  
REGISTRATION NUMBER: 32,993  
REFERENCE/DOCKET NUMBER: 135/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8614  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: 35S Promoter  
US-09-291-238-5

Query Match  
Best Local Similarity 8.7%; Score 40.4; DB 4; Length 560;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCAGACTA 307  
|||||  
Db 322 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGACAAATCCCACTA 371

RESULT 15  
US-09-330-760-5  
Sequence 5, Application us/09330760  
Patent No. 6229075  
GENERAL INFORMATION:  
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi  
TITLE OF INVENTION: DNA Construct Containing Bacillus  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6229075artis Corporation  
STREET: 564 Morris Avenue  
CITY: Summit  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07901  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/330,760  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/042,426  
FILING DATE: March 13, 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoxie, Thomas  
REGISTRATION NUMBER: 32,993  
REFERENCE/DOCKET NUMBER: 135/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8614  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:

CLONE: 35S Promoter  
US-09-330-760-5

Query Match  
Best Local Similarity 8.7%; Score 40.4; DB 4; Length 560;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCAGACTA 307  
|||||  
Db 322 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGACAAATCCCACTA 371

Search completed: April 14, 2003, 10:28:36  
Job time : 53.6289 secs



GenCore version 5.1.4 p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:29:46 ; Search time 55.567 Seconds  
(without alignments)  
7293.024 Million cell updates/sec

Title: US-09-963-803-20

Perfect score: 462  
Sequence: 1 aaagctgcatgcctgcagca.....cacacaacactagagatcc 462

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Published\_Applications\_NA.\*  
2: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
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12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID               | Description       |
|------------|-------|-------------|--------|------------------|-------------------|
| 1          | 462   | 100.0       | 462    | US-09-963-803-20 | Sequence 20, Appl |
| 2          | 373.6 | 80.9        | 600    | US-09-963-803-22 | Sequence 22, Appl |
| 3          | 354.2 | 76.7        | 541    | US-09-963-803-24 | Sequence 24, Appl |
| 4          | 314   | 68.0        | 393    | US-09-963-803-19 | Sequence 19, Appl |
| 5          | 262   | 56.7        | 604    | US-09-963-803-23 | Sequence 23, Appl |
| 6          | 240.2 | 52.0        | 392    | US-09-963-803-21 | Sequence 21, Appl |
| 7          | 212.4 | 46.0        | 317    | US-09-963-803-3  | Sequence 3, Appl  |
| 8          | 212.4 | 46.0        | 472    | US-09-963-803-25 | Sequence 25, Appl |
| 9          | 200.4 | 43.4        | 348    | US-09-963-803-4  | Sequence 4, Appl  |
| 10         | 152.8 | 33.1        | 371    | US-09-963-803-5  | Sequence 5, Appl  |
| 11         | 140.8 | 30.5        | 301    | US-09-963-803-7  | Sequence 7, Appl  |
| 12         | 140.8 | 30.5        | 398    | US-09-963-803-6  | Sequence 6, Appl  |
| 13         | 120.6 | 26.1        | 515    | US-09-963-803-2  | Sequence 2, Appl  |
| 14         | 120.6 | 26.1        | 532    | US-09-765-555-1  | Sequence 1, Appl  |
| 15         | 120.6 | 26.1        | 8340   | US-09-847-057-4  | Sequence 4, Appl  |
| 16         | 120.6 | 26.1        | 8340   | US-09-874-926-4  | Sequence 4, Appl  |
| 17         | 120.6 | 26.1        | 12241  | US-10-033-190-5  | Sequence 5, Appl  |
| 18         | 80    | 17.3        | 243    | US-09-963-803-1  | Sequence 1, Appl  |
| 19         | 75.4  | 16.3        | 392    | US-09-963-803-21 | Sequence 21, Appl |

|    |      |      |       |    |                   |                    |
|----|------|------|-------|----|-------------------|--------------------|
| 20 | 69.6 | 15.1 | 79    | 9  | US-09-963-803-14  | Sequence 14, Appl  |
| 21 | 62   | 13.4 | 62    | 9  | US-09-963-803-10  | Sequence 10, Appl  |
| 22 | 60   | 13.0 | 60    | 9  | US-09-963-803-9   | Sequence 9, Appl   |
| 23 | 60   | 13.0 | 63    | 9  | US-09-963-803-12  | Sequence 12, Appl  |
| 24 | 58   | 12.6 | 80    | 10 | US-09-870-375-34  | Sequence 34, Appl  |
| 25 | 58   | 12.6 | 236   | 10 | US-09-870-375-35  | Sequence 35, Appl  |
| 26 | 58   | 12.6 | 299   | 10 | US-09-870-375-36  | Sequence 36, Appl  |
| 27 | 58   | 12.6 | 332   | 10 | US-09-870-375-7   | Sequence 7, Appl   |
| 28 | 58   | 12.6 | 472   | 10 | US-09-870-375-5   | Sequence 5, Appl   |
| 29 | 55   | 11.9 | 65    | 9  | US-09-963-803-8   | Sequence 8, Appl   |
| 30 | 55   | 11.9 | 80    | 10 | US-09-870-375-28  | Sequence 28, Appl  |
| 31 | 45   | 9.7  | 63    | 9  | US-09-963-803-13  | Sequence 13, Appl  |
| 32 | 41.6 | 9.0  | 671   | 9  | US-10-184-644-346 | Sequence 346, Appl |
| 33 | 40.4 | 8.7  | 566   | 10 | US-09-951-470-3   | Sequence 3, Appl   |
| 34 | 40.4 | 8.7  | 661   | 10 | US-09-943-692-33  | Sequence 33, Appl  |
| 35 | 40.4 | 8.7  | 700   | 9  | US-10-138-221-9   | Sequence 9, Appl   |
| 36 | 40.4 | 8.7  | 763   | 9  | US-10-162-214-9   | Sequence 9, Appl   |
| 37 | 40.4 | 8.7  | 3983  | 9  | US-09-758-987-1   | Sequence 1, Appl   |
| 38 | 40.4 | 8.7  | 4973  | 9  | US-09-990-659A-15 | Sequence 15, Appl  |
| 39 | 40.4 | 8.7  | 5767  | 9  | US-09-810-861B-3  | Sequence 3, Appl   |
| 40 | 40.4 | 8.7  | 7129  | 9  | US-10-047-543-101 | Sequence 10, Appl  |
| 41 | 40.4 | 8.7  | 13737 | 9  | US-10-074-279-10  | Sequence 4, Appl   |
| 42 | 40.4 | 8.7  | 14446 | 9  | US-09-810-861B-4  | Sequence 33, Appl  |
| 43 | 39.2 | 8.5  | 63    | 10 | US-09-870-375-33  | Sequence 8, Appl   |
| 44 | 39.2 | 8.5  | 219   | 10 | US-09-870-375-8   | Sequence 9, Appl   |
| 45 | 39.2 | 8.5  | 282   | 10 | US-09-870-375-9   |                    |

#### ALIGNMENTS

##### RESULT 1

US-09-963-803-20  
Sequence 20, Application US/09963803  
Publication No. US20030028922A1  
GENERAL INFORMATION:  
APPLICANT: Meristem Therapeutics  
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow  
FILE REFERENCE: 184332042  
CURRENT APPLICATION NUMBER: US/09/963,803  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: FR 99/03925  
PRIOR FILING DATE: 1999-03-29  
PRIOR APPLICATION NUMBER: PCT IB00/00370  
PRIOR FILING DATE: 2000-10-05  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 20  
LENGTH: 462  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: promoter MPr1163  
NAME/KEY: promoter  
LOCATION: (1)..(462)  
OTHER INFORMATION:  
US-09-963-803-20

##### Query Match

Best Local Similarity 100.0%; Pred. No. 5.8e-129;  
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCTGATGCTGAGACAGTATGATCCGCGCTATCATGACATCATGACAGTACTGA 60  
|||||  
DB 1 AAAGCTGATGCTGAGACAGTATGATCCGCGCTATCATGACATCATGACAGTACTGA 60  
|||||  
QY 61 GGAGATGAATAGTATGACATGACATCTGTGCGAATATTTGAAGACGTAAGACATGACGAC 120  
|||||  
DB 61 GGAGATGAATAGTATGACATGACATCTGTGCGAATATTTGAAGACGTAAGACATGACGAC 120  
|||||  
QY 121 AACATGAAAAGAGAAGATTAAGTTCGCTGATTTGTGAAAGACGACATTAAGGACACATGTA 180  
|||||

|||||  
Db 121 AACATGAAAGAAAGATAGAGTGGGATGTGAAAGACATAGAGGACACATGTA 180  
OY 181 AGGTGGAATAATGTAAGGGCGGAAAGTAACCTTATGATTTGTAATTTGGTTACGACTAGT 240  
Db 181 AGGTGGAATAATGTAAGGGCGGAAAGTAACCTTATGATTTGTAATTTGGTTACGACTAGT 240  
OY 241 GATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCC 300  
Db 241 GATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCC 300  
OY 301 ACGACTAGTATGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATG 360  
Db 301 ACGACTAGTATGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATG 360  
OY 361 ACGCATGCCAGCTTACCGCGGTATGCCGTTCCCAAGCTTTATTTCTTATTTAAGCACTT 420  
Db 361 ACGCATGCCAGCTTACCGCGGTATGCCGTTCCCAAGCTTTATTTCTTATTTAAGCACTT 420  
OY 421 GTGTAGTACCTAGAAACCAACACACACACCTAGAGATCC 462  
Db 421 GTGTAGTACCTAGAAACCAACACACACACCTAGAGATCC 462

## RESULT 2

US-09-963-803-22

Sequence 22, Application US/09963803

Publication No. US20030028922A1

GENERAL INFORMATION:

APPLICANT: Meristem Therapeutics

TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow n

FILE REFERENCE: 184332042

CURRENT FILING DATE: 2001-09-26

PRIOR FILING DATE: 1999-03-29

PRIOR APPLICATION NUMBER: FR 99/03925

PRIOR FILING DATE: 1999-03-29

PRIOR APPLICATION NUMBER: PCT IB00/00370

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn version 3.1

SEQ ID NO 22

LENGTH: 600

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: promoter MP-1165

NAME/KEY: promoter

LOCATION: (1)..(600)

OTHER INFORMATION:

US-09-963-803-22

Query Match 80.9%; Score 373.6; DB 9; Length 600;

Best Local Similarity 95.3%; Pred. No. 2.2e-102;

Matches 383; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 1 AAGCTTGATGCTGCACACACTAGTATCCGCCGTCATCATATGACATCATCACTAGTCA 60  
Db 1 AAGCTTGATGCTGCACACACTAGTATCCGCCGTCATCATATGACATCATCACTAGTCA 60  
OY 61 GGAGATGAATAGCTAGCCATGACACTCTGTGCGAATATTGAAGACGTAAAGCACTAGCAG 120  
Db 61 GGAGATGAATAGCTAGCCATGACACTCTGTGCGAATATTGAAGACGTAAAGCACTAGCAG 120  
OY 121 AACATGAAAGAAAGATAGTATGCGTATGTGAANAAGACATAGAGGACACATGTA 180  
Db 121 AACATGAAAGAAAGATAGTATGCGTATGTGAANAAGACATAGAGGACACATGTA 180  
OY 181 AGGTGGAATAATGTAAGGGCGGAAAGTAACCTTATGATTTGTAATTTGGTTACGACTAGT 240  
Db 181 AGGTGGAATAATGTAAGGGCGGAAAGTAACCTTATGATTTGTAATTTGGTTACGACTAGT 240

OY 241 GATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCC 300  
Db 241 GATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCC 300  
OY 301 ACGACTAGTATGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATG 360  
Db 301 ACGACTAGTATGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATG 360  
OY 361 ACGCATGCCAGCTTACCGCGGTATGCCGTTCCCAAGCTTTATTTCTTATTTAAGCACTT 404  
Db 361 ACGCATGCCAGCTTACCGCGGTATGCCGTTCCCAAGCTTTATTTCTTATTTAAGCACTT 404

## RESULT 3

US-09-963-803-24

Sequence 24, Application US/09963803

Publication No. US20030028922A1

GENERAL INFORMATION:

APPLICANT: Meristem Therapeutics

TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow

FILE REFERENCE: 184332042

CURRENT FILING DATE: 2001-09-26

PRIOR FILING DATE: 1999-03-29

PRIOR APPLICATION NUMBER: FR 99/03925

PRIOR FILING DATE: 1999-03-29

PRIOR APPLICATION NUMBER: PCT IB00/00370

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn version 3.1

SEQ ID NO 24

LENGTH: 541

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: promoter MP-1168

NAME/KEY: promoter

LOCATION: (1)..(541)

OTHER INFORMATION:

US-09-963-803-24

Query Match 76.7%; Score 354.2; DB 9; Length 541;

Best Local Similarity 98.4%; Pred. No. 1.4e-96;

Matches 379; Conservative 0; Mismatches 3; Indels 3; Gaps 2;

OY 78 CATGACACTGTGTGGATATTGAAGAGCTAAGCACTGACGCAACATGAAAGAA 137  
Db 160 CATGCACTGTGTGGATATTGAAGAGCTAAGCACTGACGCAACATGAAAGAA 219  
OY 138 GATAAGTCTGGTATGTGAAGAGACATAGAGGACACATGTAGGTGAAATGTAAG 197  
Db 220 GATAAGTCTGGTATGTGAGAGACATAGAGGACACATGTAGGTGAAATGTAAG 278  
OY 198 GCGGAAAGTAACCTTATGATTTGTAATTTGGTTACGACTAGTATGATATGTA 257  
Db 279 GCGGAAAGTAACCTTATGATTTGTAATTTGGTTACGACTAGTATGATATGTA 338  
OY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCACAGTATGATGATG 317  
Db 339 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCACAGTATGATGATG 398  
OY 318 TGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCAGTTAAC 377  
Db 399 TGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCAGTTAAC 458  
OY 378 CGGTATGCCGGTCCCAAGCTTTATTTCTTATTTAAGCACTTGTGTAGCTTAGAA 437  
Db 459 CGGTATGCCGGTCCCAAGCTTTATTTCTTATTTAAGCTTGTGTAGCTTAGAA 516  
OY 438 ACCAACAACAACCTAGAGATCC 462  
Db 517 ACCAACAACAACCTAGAGATCC 541



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RESULT 4
US-09-963-803-19
; Sequence 19, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
; TITLE OF INVENTION: vitus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963.803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPr1162
; NAME/KEY: promoter
; LOCATION: (1)..(393)
; OTHER INFORMATION:
US-09-963-803-19
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Query Match 68.0%; Score 314; DB 9; Length 393;

Best Local Similarity 85.1%; Pred. No. 1.4e-84; Matches 393; Conservative 0; Mismatches 0; Indels 69; Gaps 1;

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QY 1 AAGTTGCATGCTGCGACGACATAGTATCCCGTCATCAATGACATCATCACTACTGA 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 AAGTTGCATGCTGCGACGACATAGTATCCCGTCATCAATGACATCATCACTACTGA 60
QY 61 GGAGATGAATAGCTAGCCATGACACTCTGTGCGAATATTGAAGCGTAAGCACTGACGAC 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 61 GGAGATGAATAGCTAGCCATGACACTCTGTGCGAATATTGAAGCGTAAGCACTGACGAC 120
QY 121 AACAAATGAAGAAGATAGGTGGTGAATGTGAAGAAGCATAGAGACATGATA 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 121 AACAAATGAAGAAGATAGGTGGTGAATGTGAAGAAGCATAGAGACATGATA 180
QY 181 AGGTGAAAATGTAAAGGCGGAAAGTAACCTTATGATTTGTAATTTGTTACGACTAGT 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 181 AGGTGAAAATGTAAAGGCGGAAAGTAACCTTATGATTTGTAATTTGTTACGACTAGT 240
QY 241 GATTGATGTATCAAGATTGATGTATCTCCACTGACGTAAAGGATGACGATGCC 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 241 GATTGATGTATCAAGATTGATGTATCTCCACTGACGTAAAGGATGACGATGCC 300
QY 301 ACAGCTAGTATGATGTATCAAGATTGATGTATCTCCACTGACGTAAAGGATG 360
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 301 ACAGCTAGTATGATGTATCAAGATTGATGTATCTCCACTGACGTAAAGGATG 360
QY 361 ACAGCTAGTATGATGTATCAAGATTGATGTATCTCCACTGACGTAAAGGATG 420
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 361 ACAGCTAGTATGATGTATCAAGATTGATGTATCTCCACTGACGTAAAGGATG 420
QY 421 GTGTAGTAGCTTAGAAAACCAACAACAACCTAGAGATCC 462
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 421 GTGTAGTAGCTTAGAAAACCAACAACAACCTAGAGATCC 462
QY 462 GTGTAGTAGCTTAGAAAACCAACAACAACCTAGAGATCC 393
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 462 GTGTAGTAGCTTAGAAAACCAACAACAACCTAGAGATCC 393
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RESULT 5
US-09-963-803-23
; Sequence 23, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
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; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; TITLE OF INVENTION: vitus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963.803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 604
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPr1167
; NAME/KEY: promoter
; LOCATION: (1)..(604)
; OTHER INFORMATION:
US-09-963-803-23
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Query Match 56.7%; Score 262; DB 9; Length 604;

Best Local Similarity 83.3%; Pred. No. 7.1e-69; Matches 375; Conservative 0; Mismatches 5; Indels 70; Gaps 4;

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QY 78 CATGACACTCTGCGAATATTGAAGACGTAAAGCATGACGACACAAATGAAAAGAA 137
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 160 CATGCCACTCTGCGAATATTGAAGACGTAAAGCATGACGACACAAATGAAAAGAA 219
QY 138 GATTAAGTCGCGTATGTAAGAGACATAGAGACATGTAAGTGGAAAATGTAAGG 197
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 138 GATTAAGTCGCGTATGTAAGAGACATAGAGACATGTAAGTGGAAAATGTAAGG 278
QY 198 GCGGAAGTAACCTTATGCAATTTGTAATTTGTAAGCAAGTATGATGATATCA 257
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 198 GCGGAAGTAACCTTATGCAATTTGTAATTTGTAAGCAAGTATGATGATATCA 336
QY 279 GCGGAAGTAACCTTATGCAATTTGTAATTTGTAAGCAAGTATGATGATATCA 336
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 279 GCGGAAGTAACCTTATGCAATTTGTAATTTGTAAGCAAGTATGATGATATCA 301
QY 258 GATTGATGTATATCTCCACTGACGTAAAGGATGACGATGCCA 301
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DB 258 GATTGATGTATATCTCCACTGACGTAAAGGATGACGATGCCA 396
QY 337 GATTGATGTATATCTCCACTGACGTAAAGGATGACGATGCCA 396
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 337 GATTGATGTATATCTCCACTGACGTAAAGGATGACGATGCCA 312
QY 302 -----CGACTAGTAT 312
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 302 -----CGACTAGTAT 456
QY 397 ATATCAAGATTGATGTATATCTCCACTGACGTAAAGGATGACGATGCCA 456
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 397 ATATCAAGATTGATGTATATCTCCACTGACGTAAAGGATGACGATGCCA 372
QY 313 TGATGTATATCAAGATTGATGTATATCTCCACTGACGTAAAGGATGACGATGCCA 372
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 313 TGATGTATATCAAGATTGATGTATATCTCCACTGACGTAAAGGATGACGATGCCA 516
QY 457 TGATGTATATCAAGATTGATGTATATCTCCACTGACGTAAAGGATGACGATGCCA 516
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 457 TGATGTATATCAAGATTGATGTATATCTCCACTGACGTAAAGGATGACGATGCCA 432
QY 373 TTACCCGGTATGCGGTTCCCAAGCTTATTTTAAAGCACTGTGTAGTACTT 432
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 373 TTACCCGGTATGCGGTTCCCAAGCTTATTTTAAAGCACTGTGTAGTACTT 516
QY 517 TTACCCGGTATGCGGTTCCCAAGCTTATTTTAAAGCACTGTGTAGTACTT 516
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 517 TTACCCGGTATGCGGTTCCCAAGCTTATTTTAAAGCACTGTGTAGTACTT 604
QY 433 AGAAACCAACACACAACTAGAGATCC 462
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DB 433 AGAAACCAACACACAACTAGAGATCC 604
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 433 AGAAACCAACACACAACTAGAGATCC 604
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RESULT 6
US-09-963-803-21
; Sequence 21, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; TITLE OF INVENTION: vitus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963.803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
```

|                       |                 |                |           |             |
|-----------------------|-----------------|----------------|-----------|-------------|
| Query Match           | 46.0%;          | Score 212.4;   | DB 9;     | Length 472; |
| Best Local Similarity | 91.5%;          | Pred. 4.8e-54; |           |             |
| Matches 236;          | Conservative 0; | Mismatches 21; | Indels 1; | Gaps 1      |

  

|    |     |   |     |
|----|-----|---|-----|
| QY | 78  | CATGCACTCTGTGGCAATATTGAAGACGTAAAGCACTGACGCAACAATGAAGAAGAA       | 137 |
|    |     |   |     |
| Db | 160 | CATGCCACTCTGTGGCAATATTGAAGACGTAAAGCACTGACGCAACAATGAAGAAGAA      | 219 |
| QY | 138 | GATAAGGTCTGGGTGATTGTGAAAAGAGACATAGAGACACATGTAAAGTGGAAAATGTAAAG  | 197 |
|    |     |   |     |
| Db | 220 | GATAAGTCTGGGTGATTGTG - AAGACACATAGAGACACATGTAAAGTGGAAAATGTAAAG  | 278 |
| QY | 198 | GCAGAAAGTAAACCTTATGCAATTTTGTAAATTTGCTTACGACTAGTATGTATGATATATCAA | 257 |



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Db      123 GATTAAGGTCGGTATTGCTG-AAGAGACATAGAGACACATGAAGTGGAATAATGTAAAG 181
QY      198 GCGGAAGTAACCTTATGATCTATTGTAATTTGGTTAC 233
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Db      182 GCGGAAGTAACCTTATGATCTATTGTAACCTTGTTAC 217

RESULT 12
US-09-963-803-6
; Sequence 6, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIORITY FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: promoter MPr1147
; LOCATION: (1)..(398)
; OTHER INFORMATION:
US-09-963-803-6

Query Match          30.5%; Score 140.8; DB 9; Length 398;
Best Local Similarity 98.1%; Pred. No. 1.4e-32;
Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY      78 CATGACACTGTGCGCAATTGTGAAGCGTAAGCAGTACAGACACATATAAAGAAGAA 137
        |||
Db      160 CATGCCACTGTGCGCAATTGTGAAGCGTAAGCAGTACAGACACATATAAAGAAGAA 219
QY      138 GATAAGTCGGTATTGTGAAGAGACATAGAGACACATGTAAAGTGGAATGTAAAG 197
        |||
Db      220 GATAAGTCGGTATTGTG-AAGAGACATAGAGACACATGTAAAGTGGAATGTAAAG 278
QY      198 GCGGAAGTAACCTTATGATCTATTGTAATTTGGTTAC 233
        |||
Db      279 GCGGAAGTAACCTTATGATCTATTGTAACCTTGTTAC 314

RESULT 13
US-09-963-803-2
; Sequence 2, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIORITY FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 515
```

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter from the intergenic region of Cassava Vein Mosaic Vi
; OTHER INFORMATION: of 515 bp in length EMBL
; FILE REFERENCE:
; NAME/KEY: promoter
; LOCATION: (1)..(515)
; OTHER INFORMATION:
US-09-963-803-2

Query Match          26.1%; Score 120.6; DB 9; Length 515;
Best Local Similarity 93.3%; Pred. No. 1.8e-26;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      93 GAATATTGAAGAGCTAAGCCTGACGCAACAATGAAGAAAGATAAGTACGTCGTGAT 152
        |||
Db      231 GAATCTTGAAGAGCTAAGCCTGACGCAACAATGAAGAAAGATAAGTACGTCGTGAT 290
QY      153 TGTGAAGAAGACATAGAGACACATGTAAAGTGAAGTGAAGGCGGAAAGTAACCTT 212
        |||
Db      291 TGTGAAGAAGACATAGAGACACATGTAAAGTGAAGTGAAGGCGGAAAGTAACCTT 350
QY      213 ATGCATTTGTAATTT 227
        |||
Db      351 ATCAACAAGGAATCT 365

RESULT 14
US-09-765-555-1
; Sequence 1, Application US/09765555
; Publication No. US20030037335A1
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: Methods and compositions to modulate
; FILE REFERENCE: 27801-20014.40
; CURRENT APPLICATION NUMBER: US/09/765,555
; PRIORITY FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 09/620,897
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,468
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 532
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter CSVWV
US-09-765-555-1

Query Match          26.1%; Score 120.6; DB 9; Length 532;
Best Local Similarity 93.3%; Pred. No. 1.8e-26;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      93 GAATATTGAAGAGCTAAGCCTGACGCAACAATGAAGAAAGATAAGTACGTCGTGAT 152
        |||
Db      231 GAATCTTGAAGAGCTAAGCCTGACGCAACAATGAAGAAAGATAAGTACGTCGTGAT 290
QY      153 TGTGAAGAAGACATAGAGACACATGTAAAGTGAAGTGAAGGCGGAAAGTAACCTT 212
        |||
Db      291 TGTGAAGAAGACATAGAGACACATGTAAAGTGAAGTGAAGGCGGAAAGTAACCTT 350
QY      213 ATGCATTTGTAATTT 227
        |||
Db      351 ATCAACAAGGAATCT 365

RESULT 15
US-09-847-057-4/c
; Sequence 4, Application US/09847057
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: Patent NO. US20020004943A1
:
: GENERAL INFORMATION:
:
: APPLICANT: AGRINOMICS, LLC.
:
: TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A PAGODA PHENOTYPE IN PLANTS
:
: FILE REFERENCE: PAGODA
:
: CURRENT APPLICATION NUMBER: US/09/847,057
:
: CURRENT FILING DATE: 2001-05-01
:
: NUMBER OF SEQ ID NOS: 4
:
: SOFTWARE: PatentIn version 3.0
:
: SEQ ID NO 4
:
: LENGTH: 8340
:
: TYPE: DNA
:
: ORGANISM: Binary vector pAG14002
:
: US-09-847-057-4

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|                           |        |                    |           |              |
|---------------------------|--------|--------------------|-----------|--------------|
| Query Match               | 26.1%; | Score 120.6;       | DB 10;    | Length 8340; |
| Best Local Similarity     | 93.3%; | Pred. No. 6.8e-26; |           |              |
| Matches 126; Conservative | 0;     | Mismatches 9;      | Indels 0; | Gaps 0;      |

|    |      |   |      |
|----|------|---|------|
| QY | 93   | GAATATTGAAGAGCTAAGCACTACACACAACATGAAAGAAGAAGATTAAGTCCGTAT   | 152  |
|    | 7853 | GAATCTTGAAGAGCTAAGCACTACACACAACATGAAAGAAGAAGATTAAGTCCGTAT   | 7794 |
| QY | 153  | TGTGAAAGAGACATAGAGGACACATGTAAAGTCGAAAAGTAAAGGCGGAAGTAACTT   | 212  |
|    | 7793 | TGTGAAAGAGACATAGAGGACACATGTAAAGTGTGAAAATGTAAAGGCGGAAGTAACTT | 7734 |
| QY | 213  | ATGCATTGTGAATTT   | 227  |
|    | 7733 | ATGCATAAGGAATCT   | 7719 |

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Search completed: April 14, 2003, 12:29:08
Job time : 58.567 secs
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GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 08:13:29 ; Search time 1863.88 Seconds

(Without alignments)  
6232.082 Million cell updates/sec

Title: US-09-963-803-20

Perfect score: 462  
Sequence: 1 aagctgcacgtcgtcagca.....cacacaacctagagatcc 462

Scoring table: IDENTITY\_NDC  
Gapop 10.0 , Gapect 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 43582208

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_NA\_Main:\*

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| 3:  | /cgn2_6/ptodata/1/pna/US07.COMB.seq:*   |
| 4:  | /cgn2_6/ptodata/1/pna/US08.COMB.seq:*   |
| 5:  | /cgn2_6/ptodata/1/pna/US081.COMB.seq:*  |
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| 43: | /cgn2_6/ptodata/1/pna/US119.COMB.seq:*  |

| Result |       | Query |        | SUMMARIES |                  | Description       |  |
|--------|-------|-------|--------|-----------|------------------|-------------------|--|
| No.    | Score | Match | Length | ID        |                  |                   |  |
| 1      | 462   | 100.0 | 462    | 36        | US-09-963-803-20 | Sequence 20, Appl |  |
| 2      | 373.6 | 80.9  | 600    | 36        | US-09-963-803-22 | Sequence 22, Appl |  |
| 3      | 354.2 | 76.7  | 541    | 36        | US-09-963-803-24 | Sequence 24, Appl |  |
| 4      | 314   | 68.0  | 341    | 36        | US-09-963-803-19 | Sequence 19, Appl |  |
| 5      | 262   | 56.7  | 604    | 36        | US-09-963-803-23 | Sequence 23, Appl |  |
| 6      | 240.2 | 52.0  | 392    | 36        | US-09-963-803-21 | Sequence 21, Appl |  |
| 7      | 212.4 | 46.0  | 317    | 36        | US-09-963-803-3  | Sequence 3, Appl  |  |
| 8      | 212.4 | 46.0  | 472    | 36        | US-09-963-803-25 | Sequence 25, Appl |  |
| 9      | 200.4 | 43.4  | 348    | 36        | US-09-963-803-4  | Sequence 4, Appl  |  |
| 10     | 152.8 | 33.1  | 371    | 36        | US-09-963-803-5  | Sequence 5, Appl  |  |
| 11     | 140.8 | 30.5  | 301    | 36        | US-09-963-803-7  | Sequence 7, Appl  |  |
| 12     | 140.8 | 30.5  | 398    | 36        | US-09-963-803-6  | Sequence 6, Appl  |  |
| 13     | 120.6 | 26.1  | 392    | 1         | PCT-US97-10376-1 | Sequence 1, Appl  |  |
| 14     | 120.6 | 26.1  | 392    | 1         | PCT-US97-10376-1 | Sequence 1, Appl  |  |
| 15     | 120.6 | 26.1  | 392    | 16        | US-09-202-838-1  | Sequence 1, Appl  |  |
| 16     | 120.6 | 26.1  | 392    | 16        | US-09-202-838-1  | Sequence 1, Appl  |  |
| 17     | 120.6 | 26.1  | 411    | 1         | PCT-US97-10376-4 | Sequence 4, Appl  |  |
| 18     | 120.6 | 26.1  | 411    | 1         | PCT-US97-10376-4 | Sequence 4, Appl  |  |
| 19     | 120.6 | 26.1  | 411    | 16        | US-09-202-838-4  | Sequence 4, Appl  |  |
| 20     | 120.6 | 26.1  | 411    | 16        | US-09-202-838-4  | Sequence 4, Appl  |  |
| 21     | 120.6 | 26.1  | 515    | 25        | US-09-641-466-1  | Sequence 1, Appl  |  |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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22 120.6 26.1 515 36 US-09-963-803-2 Sequence 2, Appl1
23 120.6 26.1 524 1 PCT-US97-10376-2 Sequence 2, Appl1
24 120.6 26.1 524 1 PCT-US97-10376A-2 Sequence 2, Appl1
25 120.6 26.1 524 16 US-09-202-838-2 Sequence 2, Appl1
26 120.6 26.1 524 16 US-09-202-838-2 Sequence 3, Appl1
27 120.6 26.1 524 16 US-09-202-838A-2 Sequence 3, Appl1
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30 120.6 26.1 526 1 PCT-US97-10376A-3 Sequence 3, Appl1
31 120.6 26.1 532 30 US-09-765-555-1 Sequence 1, Appl1
32 120.6 26.1 838 26 US-09-673-274A-19 Sequence 19, Appl1
33 120.6 26.1 853 25 US-09-641-466-2 Sequence 2, Appl1
34 120.6 26.1 1036 26 US-09-673-274A-20 Sequence 20, Appl1
35 120.6 26.1 8340 32 US-09-847-057-4 Sequence 4, Appl1
36 120.6 26.1 8340 33 US-09-847-926-4 Sequence 4, Appl1
37 120.6 26.1 12241 1 PCT-US01-50638-5 Sequence 5, Appl1
38 120.6 26.1 12241 35 US-09-948-138-4 Sequence 5, Appl1
39 120.6 26.1 12241 38 US-10-033-180-5 Sequence 5, Appl1
40 117.4 25.4 305 1 PCT-US97-10376-5 Sequence 5, Appl1
41 117.4 25.4 305 1 PCT-US97-10376A-5 Sequence 5, Appl1
42 117.4 25.4 305 16 US-09-202-838-5 Sequence 5, Appl1
43 117.4 25.4 305 16 US-09-202-838A-5 Sequence 5, Appl1
44 117.4 25.4 420 1 PCT-US97-10376-9 Sequence 9, Appl1
45 117.4 25.4 420 1 PCT-US97-10376A-9 Sequence 9, Appl1
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## ALIGNMENTS

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RESULT 1
US-09-963-803-20
: Sequence 20, Application US/09963803
: GENERAL INFORMATION:
: APPLICANT: Meristem Therapeutics
: TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
: FILE REFERENCE: 184332042
: CURRENT APPLICATION NUMBER: US/09/963,803
: CURRENT FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: FR 99/03925
: PRIOR FILING DATE: 1999-03-29
: PRIOR APPLICATION NUMBER: PCT IB00/00370
: PRIOR FILING DATE: 2000-10-05
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 20
: LENGTH: 462
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: promoter MPr1163
: NAME/KEY: promoter
: LOCATION: (1)..(462)
: OTHER INFORMATION:
US-09-963-803-20
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Query Match 100.0%; Score 462; DB 36; Length 462;

Best Local Similarity 100.0%; Pred. No. 4.4e-123;

Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AACCTTGATGCTGCAGACACTAGTATCCGCCGTCAATGACATCATCAGTACTGA 60
DB 1 AACCTTGATGCTGCAGACACTAGTATCCGCCGTCAATGACATCATCAGTACTGA 60
QY 61 GGAGATGAATAGCTAGCAGACACTGTGCGAATATTGAAGACCTAAGCAGTACGAC 120
DB 61 GGAGATGAATAGCTAGCAGACACTGTGCGAATATTGAAGACCTAAGCAGTACGAC 120
QY 121 AACCAATGAAAGAGAAGATTAAGTGCATGATTTGTAAGAGACATTAAGAGACATGTA 180
DB 121 AACCAATGAAAGAGAAGATTAAGTGCATGATTTGTAAGAGACATTAAGAGACATGTA 180
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QY 181 AGGTGGAANAATGTAAAGCGGGAAGATTAACCTTATGCAATTTGGTTAGCACTAGT 240
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QY 241 GATTGATGTGATATCAAGATTGATGTGATATCTCCACTACGTAAGGATGACGATGCC 300
DB 241 GATTGATGTGATATCAAGATTGATGTGATATCTCCACTACGTAAGGATGACGATGCC 300
QY 301 ACAGACAGATGATGATGATATCAAGATTGATGATGATATGATATGATGATGATGATG 360
DB 301 ACAGACAGATGATGATGATATCAAGATTGATGATGATGATGATGATGATGATGATG 360
QY 361 ACAGATGCAAGCTTACCGCGTATCCGTTCCCAACCTTATTTCTTATTAAGCACTT 420
DB 361 ACCGATGCCACGTTACCGCGTATCCGTTCCCAACCTTATTTCTTATTAAGCACTT 420
QY 421 GTGTAGTACCTTGAAGAACCAACACAAACCTTAAGAGATCC 462
DB 421 GTGTAGTACCTTGAAGAACCAACACAAACCTTAAGAGATCC 462
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RESULT 2
US-09-963-803-22
: Sequence 22, Application US/09963803
: GENERAL INFORMATION:
: APPLICANT: Meristem Therapeutics
: TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
: FILE REFERENCE: 184332042
: CURRENT APPLICATION NUMBER: US/09/963,803
: CURRENT FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: FR 99/03925
: PRIOR FILING DATE: 1999-03-29
: PRIOR APPLICATION NUMBER: PCT IB00/00370
: PRIOR FILING DATE: 2000-10-05
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 22
: LENGTH: 600
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: promoter MPr1165
: NAME/KEY: promoter
: LOCATION: (1)..(600)
: OTHER INFORMATION:
US-09-963-803-22
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Query Match 80.9%; Score 373.6; DB 36; Length 600;

Best Local Similarity 95.3%; Pred. No. 2.1e-97;

Matches 385; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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DB 1 AACCTTGATGCTGCAGACACTAGTATCCGCCGTCAATGACATCATCAGTACTGA 60
QY 61 GGAGATGAATAGCTAGCAGACACTGTGCGAATATTGAAGACCTAAGCAGTACGAC 120
DB 61 GGAGATGAATAGCTAGCAGACACTGTGCGAATATTGAAGACCTAAGCAGTACGAC 120
QY 121 AACCAATGAAAGAGAAGATTAAGTGCATGATTTGTAAGAGACATTAAGAGACATGTA 180
DB 121 AACCAATGAAAGAGAAGATTAAGTGCATGATTTGTAAGAGACATTAAGAGACATGTA 180
QY 181 AGGTGGAANAATGTAAAGCGGGAAGATTAACCTTATGCAATTTGGTTAGCACTAGT 240
DB 181 AGGTGGAANAATGTAAAGCGGGAAGATTAACCTTATGCAATTTGGTTAGCACTAGT 240
QY 241 GATTGATGTGATATCAAGATTGATGTGATATCTCCACTACGTAAGGATGACGATGCC 300
DB 241 GATTGATGTGATATCAAGATTGATGTGATATCTCCACTACGTAAGGATGACGATGCC 300
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;; PRIOR FILING DATE: 1999-03-29  
;; PRIOR APPLICATION NUMBER: PCT IB00/00370  
;; PRIOR FILING DATE: 2000-10-05  
;; NUMBER OF SEQ ID NOS: 39  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 23  
;; LENGTH: 604  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: promoter Mp1167  
;; NAME/KEY: promoter  
;; LOCATION: (1)..(604)  
;; OTHER INFORMATION:  
US-09-963-803-23

Query Match 56.7%; Score 262; DB 36; Length 604;  
Best Local Similarity 83.3%; Pred. No. 4, 9e-65;  
Matches 375; Conservative 0; Mismatches 5; Indels 70; Gaps 4;

QY 78 CATGACACTCTGTGCGAATATTGAGACGTAAGCACTGACGACACAAATGAAAGAA 137  
DB 160 CATGCCACTCTGTGCGAATATTGAGACGTAAGCACTGACGACACAAATGAAAGAA 219  
QY 138 GATAAGCTCGGTGATTTGTAAGAGACATAGAGACACATGTAAGGTGAAAAATGTAAG 197  
DB 220 GATAAGCTCGGTGATTTGTAAGAGACATAGAGACACATGTAAGGTGAAAAATGTAAG 278  
QY 198 GCGGAAGTAAGCTTGTGATTTGTAAGTGTAGACATAGATTTGATTTCA 257  
DB 279 GCGGAAGTAAGCTTGTGATTTGTAAGTGTAGACATAGATTTGATTTCA 336  
QY 258 GATTGATGATATCTCCACTGACGTAGAGGATGACGATGCCA----- 301  
DB 337 GATTGATGATATCTCCACTGACGTAGAGGATGACGATGCCA----- 396  
QY 302 -----CGACTAGTAT 312  
DB 397 AATCAAGATGATGATATCTCCACTGACGTAGAGGATGACGATGCCA----- 456  
QY 313 TGATGATATCAAGATTGATGATATCTCCACTGACGTAGAGGATGACGATGCCA 372  
DB 457 TGATGATATCAAGATTGATGATATCTCCACTGACGTAGAGGATGACGATGCCA 516  
QY 373 TTACCCGATATGCGGTTCCCAAGCTTTATTTCTTTATTTAAGCACTGTGTAGTCT 432  
DB 517 TTACCCGATATGCGGTTCCCAAGCTTTATTTCTTTATTTAAGCACTGTGTAGTCT 574  
QY 433 AGAAAACCAACACACACACCTAGAGATCC 462  
DB 575 AGAAAACCAACACACACACCTAGAGATCC 604

RESULT 6  
US-09-963-803-21  
;; Sequence 21, Application US/09963803  
;; GENERAL INFORMATION:  
;; APPLICANT: Meristem Therapeutics  
;; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow  
;; FILE REFERENCE: 184332042  
;; CURRENT FILING DATE: 2001-09-26  
;; PRIOR FILING DATE: 1999-03-29  
;; PRIOR APPLICATION NUMBER: PCT IB00/00370  
;; NUMBER OF SEQ ID NOS: 39  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 21  
;; LENGTH: 392  
;; TYPE: DNA

;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: promoter Mp1164  
;; NAME/KEY: promoter  
;; LOCATION: (1)..(392)  
;; OTHER INFORMATION:  
US-09-963-803-21

Query Match 52.0%; Score 240.2; DB 36; Length 392;  
Best Local Similarity 77.4%; Pred. No. 8, 9e-59;  
Matches 349; Conservative 0; Mismatches 33; Indels 69; Gaps 2;

QY 1 AAGCTTGATGCGCTGAGCACTAGTATCCCGTCATCAATGACATCATCAGTACTGA 60  
DB 1 AAGCTTGATGCGCTGAGCACTAGTATCCCGTCATCAATGACATCATCAGTACTGA 60  
QY 61 GGAGATGAATAGTACCATGACACTCTGTGCGAATATTGAAAGAGTAAAGCACTGACGAC 120  
DB 61 GGAGATGAATAGTACCATGACACTCTGTGCGAATATTGAAAGAGTAAAGCACTGACGAC 120  
QY 121 AACAAATGAAGAGAAAGATTAAGTGTGATTTGAAAGAGACATAGAGACACATGTA 180  
DB 121 AACAAATGAAGAGAAAGATTAAGTGTGATTTGAAAGAGACATAGAGACACATGTA 180  
QY 181 AGGTGAAAATGTAAAGGCGGAAAGTAACTTATGCAATTTGTAATTTGGTACGACTAGT 240  
DB 181 AGGTGAAAATGTAAAGGCGGAAAGTAACTTATGCAATTTGTAATTTGGTACGACTAGT 240  
QY 241 GATTGATGATATCAAGATTGATGATATCTCCACTGACGTAAGGATGACGATGCC 300  
DB 235 -----TGCATGCGTATGCC 250  
QY 301 ACGACTAGTATGATGATATCAAGATTGATGATATCTCCACTGACGTAAGGATG 360  
DB 251 TTACGTCAGTGGAGATATCAATCATCTTGTATTCACATC----- 291  
QY 361 ACGCATGCCAGTTACCGCGTATCCGTTCCCAAGCTTTATTTCTTTAATTTAAGCACTT 420  
DB 292 AATCACTAGTGTGATCCCGTATGCGGTTCCTTATTTCTTTAATTTAAGCACTT 351  
QY 421 GTGTAGTACTTGAAGAAACCAACACACAAAC 451  
DB 352 GTGTAGTACTTGAAGAAACCAACACACAAAC 382

RESULT 7  
US-09-963-803-3  
;; Sequence 3, Application US/09963803  
;; GENERAL INFORMATION:  
;; APPLICANT: Meristem Therapeutics  
;; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow  
;; FILE REFERENCE: 184332042  
;; CURRENT FILING DATE: 2001-09-26  
;; PRIOR FILING DATE: 1999-03-29  
;; PRIOR APPLICATION NUMBER: PCT IB00/00370  
;; PRIOR FILING DATE: 2000-10-05  
;; NUMBER OF SEQ ID NOS: 39  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 3  
;; LENGTH: 317  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Promoter Mp1116  
;; NAME/KEY: promoter  
;; LOCATION: (1)..(317)  
;; OTHER INFORMATION:  
US-09-963-803-3

OTHER INFORMATION: promoter MPr1146



Job time : 1865.88 secs



GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 08:19:51 ; Search time 365.79 Seconds

(without alignments)  
5404.014 Million cell updates/sec

Title: US-09-963-803-20

Perfect score: 462

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Scoring table: IDEMTTRY-NUC

Searched: 5824060 seqs, 2139321184 residues

Total number of hits satisfying chosen parameters: 11648120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_NA\_New:\*  
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11: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 120.6 | 26.1        | 532    | 6     | US-09-765-555A-1  |
| 2          | 120.6 | 26.1        | 838    | 6     | US-09-673-274B-19 |
| 3          | 120.6 | 26.1        | 1036   | 6     | US-09-673-274B-20 |
| 4          | 40.4  | 8.7         | 309    | 8     | US-10-380-935-30  |
| 5          | 40.4  | 8.7         | 522    | 8     | US-10-380-935-37  |
| 6          | 40.4  | 8.7         | 835    | 8     | US-10-391-414-10  |
| 7          | 40.4  | 8.7         | 1683   | 11    | US-60-434-166-147 |
| 8          | 40.4  | 8.7         | 2361   | 9     | US-10-302-267-1   |
| 9          | 40.4  | 8.7         | 3212   | 9     | US-10-130-150-13  |
| 10         | 40.4  | 8.7         | 3288   | 9     | US-10-130-150-18  |
| 11         | 40.4  | 8.7         | 3329   | 9     | US-10-130-150-15  |
| 12         | 40.4  | 8.7         | 5247   | 9     | US-10-160-764-40  |
| 13         | 40.4  | 8.7         | 5250   | 9     | US-10-160-764-4   |
| 14         | 40.4  | 8.7         | 5511   | 9     | US-10-160-764-48  |
| 15         | 40.4  | 8.7         | 5715   | 9     | US-10-160-764-52  |
| 16         | 40.4  | 8.7         | 5796   | 8     | US-10-378-810-2   |
| 17         | 40.4  | 8.7         | 6285   | 9     | US-10-160-764-42  |
| 18         | 40.4  | 8.7         | 6299   | 9     | US-10-160-764-50  |
| 19         | 40.4  | 8.7         | 8349   | 9     | US-10-198-478-16  |
| 20         | 40.4  | 8.7         | 10249  | 9     | US-10-198-478-14  |
| 21         | 40.4  | 8.7         | 10312  | 9     | US-10-198-478-15  |
| 22         | 40.4  | 8.7         | 10339  | 9     | US-10-198-478-13  |

|   |    |      |     |        |   |                     |                   |
|---|----|------|-----|--------|---|---------------------|-------------------|
| c | 23 | 40.4 | 8.7 | 13737  | 6 | US-09-538-414-10    | Sequence 10, App1 |
|   | 24 | 39.8 | 8.6 | 250715 | 7 | US-09-949-016-13294 | Sequence 13294, A |
|   | 25 | 38.8 | 8.4 | 206    | 9 | US-10-204-889-9     | Sequence 9, App1  |
|   | 26 | 38.8 | 8.4 | 382    | 1 | PCT-US02-17853-22   | Sequence 22, App1 |
|   | 27 | 38.8 | 8.4 | 842    | 1 | US-10-321-434-6     | Sequence 6, App1  |
|   | 28 | 38.8 | 8.4 | 2267   | 1 | PCT-US02-17853-11   | Sequence 11, App1 |
|   | 29 | 38.8 | 8.4 | 2873   | 1 | PCT-US03-03435-55   | Sequence 55, App1 |
|   | 30 | 38.8 | 8.4 | 2873   | 9 | US-10-353-454-38    | Sequence 38, App1 |
|   | 31 | 38.8 | 8.4 | 2873   | 9 | US-10-356-088-55    | Sequence 55, App1 |
|   | 32 | 38.8 | 8.4 | 3002   | 9 | US-10-353-454-57    | Sequence 57, App1 |
|   | 33 | 38.8 | 8.4 | 3034   | 1 | PCT-US03-03435-48   | Sequence 48, App1 |
|   | 34 | 38.8 | 8.4 | 3034   | 9 | US-10-353-454-31    | Sequence 31, App1 |
|   | 35 | 38.8 | 8.4 | 3034   | 9 | US-10-356-088-48    | Sequence 48, App1 |
|   | 36 | 38.8 | 8.4 | 4182   | 5 | US-09-921-922A-7    | Sequence 7, App1  |
|   | 37 | 38.8 | 8.4 | 5449   | 1 | PCT-US03-03435-57   | Sequence 57, App1 |
|   | 38 | 38.8 | 8.4 | 5449   | 9 | US-10-353-454-40    | Sequence 40, App1 |
|   | 39 | 38.8 | 8.4 | 5449   | 9 | US-10-356-088-57    | Sequence 57, App1 |
|   | 40 | 38.8 | 8.4 | 6975   | 6 | US-09-464-528C-17   | Sequence 17, App1 |
|   | 41 | 38.8 | 8.4 | 9555   | 5 | US-09-921-922A-6    | Sequence 6, App1  |
|   | 42 | 38.8 | 8.4 | 13199  | 9 | US-10-137-325A-2    | Sequence 2, App1  |
| c | 43 | 38.8 | 8.4 | 17476  | 8 | US-10-385-546-7     | Sequence 7, App1  |
|   | 44 | 37   | 8.0 | 5195   | 9 | US-10-311-455-893   | Sequence 893, App |
|   | 45 | 37   | 8.0 | 6944   | 9 | US-10-311-506-113   | Sequence 113, App |

#### ALIGNMENTS

RESULT 1  
US-09-765-555A-1  
; Sequence 1, Application US/09765555A  
; GENERAL INFORMATION:  
; APPLICANT: The Scripps Research Institute  
; APPLICANT: Barbas, Carlos  
; APPLICANT: Stege, Justin  
; APPLICANT: Guan, Xueni  
; APPLICANT: Dalmia, Bipin  
; TITLE OF INVENTION: Methods and compositions to modulate  
; FILE REFERENCE: expression in plants  
; CURRENT APPLICATION NUMBER: 27801-20014.20  
; CURRENT FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: 09/620,897  
; PRIOR FILING DATE: 2000-07-21  
; PRIOR APPLICATION NUMBER: US 60/177,468  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 532  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Promoter Csywv  
US-09-765-555A-1  
Query Match 26.1%; Score 120.6; DB 6; Length 532;  
Best local similarity 93.3%; Pred. No. 1.4e-25;  
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| QY | 93  | GAATATTGAGACGTAAAGCCTGACGACACATGAAAAAGAAAGCAATAGTCGCGAT  | 132 |
| DB | 231 | GAATCTTGAAGACGTAAAGCCTGACGACACATGAAAAAGAAAGCAATAGTCGCGAT | 290 |
| QY | 153 | TGTGAAAGACATAGACACATGTAAGTGAATATTAAGCGCGAAATTAACCTT      | 212 |
| DB | 291 | TGTGAAAGACATAGACACATGTAAGTGAATATTAAGCGCGAAATTAACCTT      | 350 |
| QY | 213 | ATGCATTGTAAATTT  | 227 |
| DB | 351 | ATGCATTGTAAATTT  | 365 |

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: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: Synthetic oligonucleotide
: FEATURE:
: NAME/KEY: Promoter
: LOCATION: (7)...(532)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (539)..(736)
: FEATURE:
: NAME/KEY: terminator
: LOCATION: (767)...(1030)
US-09-673-274B-20

Query Match          26.1%; Score 120.6; DB: 6; Length 1036;
Best Local Similarity 93.38; Pred. No. 1.7e-25;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY   93 GAATATTGAAACAGCTAAGCACTGACGACACAAATGAAGAAGAAGATAAGTCGTGAT 152
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB   222 GAATCTTGAAGACGTAACACTGACGACACAAATGAAGAAGAAGATAAGTCGTGAT 281

OY   153 TGTGAAGAAGCATAGAGACACATGTAAGTCGAAAAATGTAAGGGCGGAAAGTAACCTT 212
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB   282 TGTGAAGAAGCATAGAGACACATGTAAGTGAAAATGTAAGGGCGGAAAGTAACCTT 341

OY   213 ATGCATTTGTAAATT 227
      || | || |
DB   342 ATCACAAGAAGATCT 356

RESULT 4
US-10-380-935-30
: Sequence 30, Application US/10380935
: GENERAL INFORMATION:
: APPLICANT: WARNER, Simon, Anthony, James
: APPLICANT: HARKES, Timothy, Robert
: TITLE OF INVENTION: HERBICIDE RESISTANT PLANTS
: FILE REFERENCE: PPD50594/MO
: CURRENT APPLICATION NUMBER: US/10/380.935
: CURRENT FILING DATE: 2003-03-19
: PRIOR APPLICATION NUMBER: GB0023911.1
: PRIOR FILING DATE: 2000-09-29
: PRIOR APPLICATION NUMBER: GB0027693.1
: PRIOR FILING DATE: 2000-11-13
: PRIOR APPLICATION NUMBER: GB0023910.3
: PRIOR FILING DATE: 2000-09-29
: NUMBER OF SEQ ID NOS: 70
: SOFTWARE: PatentIn version 3.1
SEQ ID NO 30
LENGTH: 309
TYPE: DNA
ORGANISM: Cauliflower Mosaic Virus
FEATURE:
OTHER INFORMATION: Enhancer
US-10-380-935-30

Query Match          8.7%; Score 40.4; DB: 8; Length 309;
Best Local Similarity 88.0%; Pred. No. 0.071;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY   258 GATGATGATGATATCTCCACTGAGTAGGATGATGCGATGCCAGGACTA 307
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB   242 GATGATGATGATATCTCCACTGAGTAGGATGATGCGATGCCAGGACTA 291

RESULT 5
US-10-380-935-37
: Sequence 37, Application US/10380935
: GENERAL INFORMATION:
: APPLICANT: WARNER, Simon, Anthony, James
: APPLICANT: HARKES, Timothy, Robert

```



```

; APPLICANT: ANDREWS, Christopher, John
; TITLE OF INVENTION: HERBICIDE RESISTANT PLANTS
; FILE REFERENCE: PPD050594/WO
; CURRENT APPLICATION NUMBER: US/10/380,935
; CURRENT FILING DATE: 2003-03-19
; PRIOR APPLICATION NUMBER: GB0023911.1
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: GB0027693.1
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: GB0023910.3
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Figwort Mosaic Virus
; FEATURE:
; OTHER INFORMATION: Enhancer
US-10-380-935-37
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```

Query Match          8.7%; Score 40.4; DB 8; Length 522;
Best Local Similarity 88.0%; Pred. No. 0.083;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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```
OY 258 GATTGATGATATCTCCACGTGACGTAAGGATGATGACGATGCCACGACTA 307
DB 459 GATTGATGATATCTCCACGTGACGTAAGGATGATGACGATGCCACGACTA 508
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RESULT 6
US-10-391-414-10
; Sequence 10, Application US/10391414
; GENERAL INFORMATION:
; APPLICANT: SHINOZAKI, Kazuko
; APPLICANT: KATSURA, Koji
; APPLICANT: ITO, Yusuke
; TITLE OF INVENTION: Stress Induced Promoter Derived From Rice
; FILE REFERENCE: 382.1041
; CURRENT APPLICATION NUMBER: US/10/391,414
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: JP 2002-377316
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 835
; TYPE: DNA
; ORGANISM: Cauliflower mosaic virus
US-10-391-414-10
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```

Query Match          8.7%; Score 40.4; DB 8; Length 835;
Best Local Similarity 88.0%; Pred. No. 0.096;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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```
OY 258 GATTGATGATATCTCCACGTGACGTAAGGATGATGACGATGCCACGACTA 307
DB 729 GATTGATGATATCTCCACGTGACGTAAGGATGATGACGATGCCACGACTA 778
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RESULT 7
US-60-434-166-147
; Sequence 147, Application US/60434166
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology
; APPLICANT: Creelman, Robert A.
; APPLICANT: Haake, Volker
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Adam, Luc J.
; APPLICANT: Jlang, Cai-Zhong
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Riechmann, Jose Luis
```

```

; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0051 P
; CURRENT APPLICATION NUMBER: US/60/434,166
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 559
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 147
; LENGTH: 1683
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G2227
US-60-434-166-147
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Query Match          8.7%; Score 40.4; DB 11; Length 1683;
Best Local Similarity 88.0%; Pred. No. 0.12;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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```
OY 258 GATTGATGATATCTCCACGTGACGTAAGGATGATGACGATGCCACGACTA 307
DB 9 GATTGATGATATCTCCACGTGACGTAAGGATGATGACGATGCCACGACTA 58
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RESULT 8
US-10-302-267-1
; Sequence 1, Application US/10302267
; GENERAL INFORMATION:
; APPLICANT: Keddle, James
; APPLICANT: Fromm, Michael
; APPLICANT: Heard, Jacqueline
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Adam, Luc
; APPLICANT: Broun, Pierre
; APPLICANT: Pineda, Omaira
; APPLICANT: Reuber, Lynne
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Jlang, Cai-Zhong
; APPLICANT: Samaha, Raymond
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Creelman, Robert
; TITLE OF INVENTION: PLANT GENE SEQUENCES II
; FILE REFERENCE: MBI-0007
; CURRENT APPLICATION NUMBER: US/10/302,267
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US/09/506,720
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/120,880
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/121,037
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: 60/124,278
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: 60/129,450
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/135,134
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 60/144,153
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: 60/161,143
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/162,656
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 218
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2361
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (144)..(2024)
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; OTHER INFORMATION: G274
US-10-302-267-1
Query Match
Best Local Similarity 8.7%; Score 40.4; DB 9; Length 2361;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 258 GATTGATGTGATATCTCCAGCTAGAGGATGATGACGATGCCAGCACTA 307
Db 113 GATTGATGTGATATCTCCAGCTAGAGGATGATGACGATGCCAGCACTA 162

RESULT 9
US-10-130-150-13
; Sequence 13, Application US/10130150
; GENERAL INFORMATION:
; APPLICANT: Shoseyov, Oded
; TITLE OF INVENTION: ASPERGILLUS NIGER BETA-GLUCOSIDASE GENE, PROTEIN AND USES THEREOF
; FILE REFERENCE: 02/23831
; CURRENT APPLICATION NUMBER: US/10/130.150
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 3212
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of recombinant construct expressing BglI protein
US-10-130-150-13

Query Match
Best Local Similarity 8.7%; Score 40.4; DB 9; Length 3212;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 258 GATTGATGTGATATCTCCAGCTAGAGGATGATGACGATGCCAGCACTA 307
Db 197 GATTGATGTGATATCTCCAGCTAGAGGATGATGACGATGCCAGCACTA 246

RESULT 10
US-10-130-150-18
; Sequence 18, Application US/10130150
; GENERAL INFORMATION:
; APPLICANT: Shoseyov, Oded
; TITLE OF INVENTION: ASPERGILLUS NIGER BETA-GLUCOSIDASE GENE, PROTEIN AND USES THEREOF
; FILE REFERENCE: 02/23831
; CURRENT APPLICATION NUMBER: US/10/130.150
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 3288
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of recombinant construct expressing BglI protein fused t
US-10-130-150-18

Query Match
Best Local Similarity 8.7%; Score 40.4; DB 9; Length 3288;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 258 GATTGATGTGATATCTCCAGCTAGAGGATGATGACGATGCCAGCACTA 307
Db 197 GATTGATGTGATATCTCCAGCTAGAGGATGATGACGATGCCAGCACTA 246

RESULT 11
US-10-130-150-15
; Sequence 15, Application US/10130150
; GENERAL INFORMATION:
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```
; APPLICANT: Shoseyov, Oded
; TITLE OF INVENTION: ASPERGILLUS NIGER BETA-GLUCOSIDASE GENE, PROTEIN AND USES THER
; FILE REFERENCE: 02/23831
; CURRENT APPLICATION NUMBER: US/10/130.150
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 3329
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of recombinant construct expressing BglI protein fuse
US-10-130-150-15

Query Match
Best Local Similarity 8.7%; Score 40.4; DB 9; Length 3329;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 258 GATTGATGTGATATCTCCAGCTAGAGGATGATGACGATGCCAGCACTA 307
Db 197 GATTGATGTGATATCTCCAGCTAGAGGATGATGACGATGCCAGCACTA 246

RESULT 12
US-10-160-764-40
; Sequence 40, Application US/10160764
; GENERAL INFORMATION:
; APPLICANT: Huang, Yafan
; APPLICANT: Chailifoux, Maryse
; APPLICANT: Wang, Yang
; APPLICANT: Kuzma, Monika Maria
; APPLICANT: Gilley, Angela Patricia
; TITLE OF INVENTION: Compositions and Methods of Increasing Stress Tolerance
; FILE REFERENCE: 22542-008
; CURRENT APPLICATION NUMBER: US/10/160.764
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,766
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/348,909
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 40
; LENGTH: 5247
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
US-10-160-764-40

Query Match
Best Local Similarity 8.7%; Score 40.4; DB 9; Length 5247;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 258 GATTGATGTGATATCTCCAGCTAGAGGATGATGACGATGCCAGCACTA 307
Db 3209 GATTGATGTGATATCTCCAGCTAGAGGATGATGACGATGCCAGCACTA 3258

RESULT 13
US-10-160-764-4
; Sequence 4, Application US/10160764
; GENERAL INFORMATION:
; APPLICANT: Huang, Yafan
; APPLICANT: Chailifoux, Maryse
; APPLICANT: Wang, Yang
; APPLICANT: Kuzma, Monika Maria
; APPLICANT: Gilley, Angela Patricia
; TITLE OF INVENTION: Compositions and Methods of Increasing Stress Tolerance
```

```
; TITLE OF INVENTION: In Plants
; FILE REFERENCE: 22542-008
; CURRENT APPLICATION NUMBER: US/10/160,764
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,766
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/348,909
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 5250
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
US-10-160-764-4

Query Match
Best Local Similarity 8.7%; Score 40.4; DB 9; Length 5250;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCATGCCACGACTA 307
      |||||||||||||||||||||||||||||||||||||||
Db 3209 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCACATCCACTA 3258

RESULT 14
US-10-160-764-48
; Sequence 48, Application US/10160764
; GENERAL INFORMATION:
; APPLICANT: Huang, Yafan
; APPLICANT: Chailfoux, Maryse
; APPLICANT: Wang, Yang
; APPLICANT: Kuzma, Monika Maria
; APPLICANT: Gilley, Angela Patricia
; TITLE OF INVENTION: Compositions and Methods of Increasing Stress Tolerance
; TITLE OF INVENTION: In Plants
; FILE REFERENCE: 22542-008
; CURRENT APPLICATION NUMBER: US/10/160,764
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,766
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/348,909
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 5511
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
US-10-160-764-48

Query Match
Best Local Similarity 8.7%; Score 40.4; DB 9; Length 5511;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCATGCCACGACTA 307
      |||||||||||||||||||||||||||||||||||||||
Db 3209 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCACATCCACTA 3258

RESULT 15
US-10-160-764-52
; Sequence 52, Application US/10160764
; GENERAL INFORMATION:
; APPLICANT: Huang, Yafan
; APPLICANT: Chailfoux, Maryse
; APPLICANT: Wang, Yang
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; APPLICANT: Kuzma, Monika Maria
; APPLICANT: Gilley, Angela Patricia
; TITLE OF INVENTION: Compositions and Methods of Increasing Stress Tolerance
; TITLE OF INVENTION: In Plants
; FILE REFERENCE: 22542-008
; CURRENT APPLICATION NUMBER: US/10/160,764
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,766
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/348,909
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 5715
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
US-10-160-764-52

Query Match
Best Local Similarity 8.7%; Score 40.4; DB 9; Length 5715;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCATGCCACGACTA 307
      |||||||||||||||||||||||||||||||||||||||
Db 3209 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGCACATCCACTA 3258
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Search completed: April 14, 2003, 12:27:40  
Job time : 377.79 secs



GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 06:53:52 ; Search time 1073.87 Seconds  
(without alignments)  
6967.603 Million cell updates/sec

Title: US-09-963-803-20

Perfect score: 462  
Sequence: 1 aagcttgatgcctgcagca.....cacacaacctagagatcc 462

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estlmu:\*  
5: em\_estlov:\*  
6: em\_estlpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_estl1:\*  
10: gb\_estl2:\*  
11: gb\_hlc:\*  
12: gb\_estl3:\*  
13: gb\_estl4:\*  
14: gb\_estl5:\*  
15: em\_estfun:\*  
16: em\_estlom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pin:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_tod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 43.8  | 9.5         | 224    | 17 | BH746858    |
| 2          | 42.4  | 9.2         | 561    | 13 | BM162517    |
| 3          | 41.8  | 9.0         | 964    | 9  | AL529655    |
| 4          | 41.8  | 9.0         | 1101   | 17 | CNS0039G    |
| 5          | 41    | 8.9         | 222    | 13 | BM161725    |
| 6          | 40.4  | 8.7         | 112    | 17 | BH751161    |

|    |      |     |     |    |          |
|----|------|-----|-----|----|----------|
| 7  | 40.4 | 8.7 | 142 | 17 | BH749349 |
| 8  | 40.4 | 8.7 | 153 | 17 | BH619283 |
| 9  | 40.4 | 8.7 | 153 | 17 | BH747013 |
| 10 | 40.4 | 8.7 | 158 | 17 | BH748291 |
| 11 | 40.4 | 8.7 | 165 | 17 | BH747357 |
| 12 | 40.4 | 8.7 | 175 | 17 | BH746616 |
| 13 | 40.4 | 8.7 | 177 | 17 | BH802465 |
| 14 | 40.4 | 8.7 | 190 | 17 | BH752801 |
| 15 | 40.4 | 8.7 | 193 | 17 | BH752801 |
| 16 | 40.4 | 8.7 | 214 | 17 | BH748289 |
| 17 | 40.4 | 8.7 | 215 | 17 | BH747829 |
| 18 | 40.4 | 8.7 | 219 | 17 | BH753813 |
| 19 | 40.4 | 8.7 | 220 | 17 | BH747744 |
| 20 | 40.4 | 8.7 | 221 | 17 | BH747438 |
| 21 | 40.4 | 8.7 | 230 | 17 | BH802415 |
| 22 | 40.4 | 8.7 | 230 | 17 | BH746474 |
| 23 | 40.4 | 8.7 | 237 | 17 | BH799173 |
| 24 | 40.4 | 8.7 | 237 | 17 | BH802463 |
| 25 | 40.4 | 8.7 | 244 | 17 | BH746375 |
| 26 | 40.4 | 8.7 | 248 | 17 | BH754798 |
| 27 | 40.4 | 8.7 | 251 | 17 | BH750171 |
| 28 | 40.4 | 8.7 | 254 | 17 | BH748500 |
| 29 | 40.4 | 8.7 | 256 | 17 | BH748499 |
| 30 | 40.4 | 8.7 | 261 | 17 | BH802470 |
| 31 | 40.4 | 8.7 | 268 | 17 | BH802493 |
| 32 | 40.4 | 8.7 | 269 | 17 | BH611919 |
| 33 | 40.4 | 8.7 | 269 | 17 | BH211646 |
| 34 | 40.4 | 8.7 | 271 | 17 | BH802489 |
| 35 | 40.4 | 8.7 | 272 | 17 | BH799178 |
| 36 | 40.4 | 8.7 | 274 | 17 | BH802428 |
| 37 | 40.4 | 8.7 | 279 | 17 | BH802495 |
| 38 | 40.4 | 8.7 | 281 | 17 | BH748475 |
| 39 | 40.4 | 8.7 | 281 | 17 | BH750170 |
| 40 | 40.4 | 8.7 | 284 | 17 | BH802443 |
| 41 | 40.4 | 8.7 | 284 | 17 | BH213307 |
| 42 | 40.4 | 8.7 | 286 | 17 | BH746665 |
| 43 | 40.4 | 8.7 | 286 | 17 | BH747007 |
| 44 | 40.4 | 8.7 | 293 | 17 | BH610310 |
| 45 | 40.4 | 8.7 | 296 | 17 | BH213532 |
|    |      |     | 335 | 17 | BH213230 |

## ALIGNMENTS

RESULT 1  
LOCUS BH746858  
DEFINITION 224 bp DNA linear GSS 27-FEB-2002  
SALK\_003694.51.40.x Arabidopsis thaliana TMDN insertion lines  
Arabidopsis thaliana genomic clone SALK\_003694.51.40.x. DNA  
sequence.

ACCESSION BH746858  
VERSION BH746858.1  
KEYWORDS GI:18959973  
SOURCE GSS.

ORGANISM thale cress.  
Arabidopsis thaliana

REFERENCE  
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadlinab,  
C., Jeske,A., Kanes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,  
Zimmerman,J., and Ecker,J.R.  
A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
Unpublished (2001)  
Contact: Joseph R. Ecker

TITLE  
JOURNAL  
COMMENT Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: eckere@salk.edu

This is single pass sequence recovered from the left border of

location="variables  
1..561  
/organism="Plasmodium yoelli yoelli"  
/strain="17XL"  
/db\_xref="taxon:73239"  
/clone="PYCKR64"  
/clone\_1lb="PYBS"  
/dev\_stage="Asexual blood stages"  
/lab\_host="E. coli XL-1 Blue"  
/note="Vector: pMD-GAL4; At 20-25% parasitemia, blood was  
collected from BALB/cBYJ mice infected with Py17XL  
parasites, and leukocytes removed by passage over  
microcrystalline cellulose columns. Total RNA was  
isolated using the guanidinium isothiocyanate method,  
RNA isolated using oligo(dT)-cellulose chromatography.

BASE COUNT 257 a 228 c 259 g 215 t 5 others  
ORIGIN

|            |            |  |           |
|------------|------------|--|-----------|
| OY         | 118        | GACAAATGAAAAGACAGATAAGTCGGTGAATTGTGAAAAGACACTAGACACACAT  | 177       |
| Db         | 758        | RWADRTWDRODDDDRRDRAGTAGRKMWRPTWKRRMRRDTPMDADADDTARDRRRRRDD   | 699       |
| OY         | 178        | GTAAGGTGGAANAATGTAAGGGCGGAACTAACCTATCATTTTGTAATTTGGTTACGACT  | 237       |
| Db         | 698        | GADKCKKKTKGTRRRRRRRAATWDRDAMWADMTTDTDDTDKDRKRGRARRRR   | 639       |
| OY         | 238        | AGTGAATGATGATATCAAGATTGATGTGATATCCACGACGACGTAAGGATGACGCAT  | 297       |
| Db         | 638        | TTRARAWMWTFWAKAMDMAKMKMTFADRWDSRADDTWTWDARKADDMAKARAWRRRRA   | 579       |
| OY         | 298        | GCCACGACTACTGATGTGATGTGATATCAAGATTGATGTGATATCT   | 342       |
| Db         | 578        | RAARADRRTTKGKTATTATTTWAARAAMWAMAATTTATWT TT  | 534       |
| RESULT 5   |            |  |           |
| LOCUS      | BM161725   |  |           |
| DEFINITION | BM161725   | 222 bp mRNA linear EST 04-DEC-2001   |           |
| ACCESSION  | EST564248  | PYBS Plasmodium yoelii yoeiii cDNA clone PYCk131 5' end,   |           |
| VERSION    | BM161725   | mRNA sequence.   |           |
| KEYWORDS   | BM161725.1 | GI:17307406  |           |
| SOURCE     |            | EST.   |           |
| ORGANISM   |            | Plasmodium yoelii yoeiii.  |           |
| REFERENCE  |            | Plasmodium yoelii yoeiii   |           |
| AUTHORS    |            | Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.  |           |
| JOURNAL    |            | 1 (bases 1 to 222)   |           |
| COMMENT    |            | Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Valdivia,A.B.,<br>Fraser,C.M. and Carucci,D.J.<br>Plasmodium yoelii EST project at TIGR<br>Unpublished (2001)<br>Contact: Jane Carlton<br>Parasite Genomics Group<br>The Institute for Genomic Research<br>9712 Medical Center Drive, Rockville, MD 20850, USA<br>Tel: 301-530-9319<br>Fax: 301-838-0208<br>Email: carlton@tigr.org<br>For clone info, please contact the Malaria Research and Reference<br>Reagent Resource Center, ATCC<br><a href="http://www.malaria.mr4.org/mr4pages/index.html">http://www.malaria.mr4.org/mr4pages/index.html</a><br>Seq primer: ADF.   |           |
| FEATURES   |            |  |           |
| source     |            | location/Qualifiers  |           |
|            |            | 1..222   |           |
|            |            | /organism="Plasmodium yoelii yoeiii"   |           |
|            |            | /strain="17XL"   |           |
|            |            | /db_xref="taxon:73239"   |           |
|            |            | /clone="PYCk131"   |           |
|            |            | /clone_lib="pyBS"  |           |
|            |            | /dev_stage="asexual blood stages"  |           |
|            |            | /lab_host="E. coli XL-1 Blue"  |           |
|            |            | /note="Vector: PAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cBYJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose columns. Total RNA was isolated using the guanidium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to Hybridzap arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (PAD-GAL4) was excised from the Hybridzap vector and plasmid DNA isolated." |           |
| BASE COUNT | 99 a       | 25 c   | 38 g 60 t |
| ORIGIN     |            |  |           |

[illegible]

RESULT 6  
BH751161  
LOCUS  
DEFINITION  
112 bp DNA linear GSS 27-FEB-2002  
SALK\_049464.49.75.x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_049464.49.75.x, DNA  
sequence.  
ACCESSION  
BH751161  
VERSION  
BH751161.1 GI:18968302  
KEYWORDS  
GSS.  
SOURCE  
thale cress.  
ORGANISM  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eucosids II; Brassicales; Brassicaceae; Arabidopsids.  
1 (bases 1 to 112)  
REFERENCE  
Alonso J.M., Leisec.T.J., Barajas,P., Chen,H., Cheuk,R., Gaarriab  
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,  
Zimmerman,J. and Ecker,J.R.  
A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
Unpublished (2001)  
JOURNAL  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
COMMENT  
This is single pass sequence recovered from the left border of  
TDNA.  
Class: TDNA tagged.

| FEATURES   | source              |
|--|---------------------|
| location/Qualifiers  | 1. 112              |
| /organism="Arabidopsis thaliana"   |                     |
| /strain="Columbia 0"   |                     |
| /db_xref="taxon:3702"  |                     |
| /clone="SALK_049464.49.75.x"   |                     |
| /clone.lib="Arabidopsis thaliana TDNA insertion lines"   |                     |
| /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at <a href="http://signal.salk.edu/cdna_protocols.html">http://signal.salk.edu/cdna_protocols.html</a> " |                     |
| BASE COUNT   | 31 a 26 c 25 g 30 t |
| ORIGIN   |                     |

|    | Query Match  | 8.7%           | Score 40.4    | DB 17    | Length 112 |
|----|--|----------------|---------------|----------|------------|
|    | Best Local Similarity                                    | 88.0%          | Pred. No. 2.8 |          |            |
|    | Matches 44   | Conservative 0 | Mismatches 6  | Indels 0 | Gaps 0     |
| OY | 258 GATTGATCTCATATCTCCACCTGAGCTTAAGGGATGACGCATGCCACGACTA | 307            |               |          |            |
| Db | 3 GATTGATGATGATATCTCCACCTGAGCTTAAGGGATGACGCACATCCCACTA   | 52             |               |          |            |

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RESULT 7
LOCUS BH749349
DEFINITION BH749349 142 bp DNA linear GSS 27-FEB-2002
ACCESSION SALK_047736.48.15.x Arabidopsis thaliana TDNA insertion lines
VERSION BH749349 Arabidopsis thaliana genomic clone SALK_047736.48.15.x, DNA
KEYWORDS sequence.
SOURCE BH749349.1 GI:18964144
ORGANISM GSS.
thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 142)
Alonso,J.M., Leisse,T.J., Baccetas,P., Chen,H., Cheuk,R., Gadrianab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
A sequence-indexed library of insertion mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel.: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1..142

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BASE COUNT  
ORIGIN

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41 a      36 c      30 g      35 t  
be found at http://signal.salk.edu/xdna\_protocols.html"  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
/organism="Arabidopsis thaliana"  
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each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at http://signal.salk.edu/xdna\_protocols.html"
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| Query Match           | 8.7%   | Score 40.4    | DB 17        | Length 142 |
|-----------------------|--|---------------|--------------|------------|
| Best Local Similarity | 88.0%  | Pred. No. 2.9 |              |            |
| Matches 44            | Conservative   | 0             | Mismatches 6 | Indels 0   |
|                       |  |               | Gaps         | 0          |
| Qy 258                | GATGATGTGATATCTCCACTGACGTAGGAGATGACCATGCCACGACTA                   | 307           |              |            |
|                       |  |               |              |            |
| Db 33                 | GATGATGTGATATCTCCACTGACGTAGGAGATGACCATGCCACACTA                    | 82            |              |            |
| RESULT 8              |  |               |              |            |
| BH619283/c            |  |               |              |            |
| LOCUS                 | BH619283   | 153 bp        | DNA          | linear     |
| DEFINITION            | SMUK_040762 Arabidopsis thaliana TDNA insertion 1lines Arabidopsis |               |              |            |
|                       | thaliana genomic clone SMUK_040762, DNA sequence.                  |               |              |            |
| ACCESSION             | BH619283   |               |              |            |
| VERSION               | BH619283.1   | GI:18429799   |              |            |

ORGANISM  
Arabidopsis thaliana  
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
Rosidae: eustosids: F1, Brassicales, Brassicaceae, Arabidopsi.s.  
1 (bases 1 to 153)  
REFERENCE  
AUTHORS  
Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab  
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.



TITLE 'Zimmerman, J. and Ecker, J.R.  
A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
Unpublished (2001)  
JOURNAL  
COMMENT Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: eckersalk.edu  
This is single pass sequence recovered from the left border of  
TDNA.  
Class: TDNA tagged.  
FEATURES  
source Location/Qualifiers  
1..153  
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/db\_xref="taxon:3702"  
/clone="SALK\_040762"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"  
BASE COUNT 36 a 34 c 36 g 47 t  
ORIGIN  
Query Match 8.7%; Score 40.4; DB 17; Length 153;  
Best Local Similarity 88.0%; Pred. No. 2.9;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 258 GATTGATGATATCTCCACTGACGTAAAGGATGACGACGACGACTA 307  
|||||  
Db 110 GATTGATGATATCTCCACTGACGTAAAGGATGACGACGACGACTA 61  
|||||  
RESULT 9  
BH747013 153 bp DNA linear GSS 27-FEB-2002  
LOCUS SALK\_008070.43.05 x Arabidopsis thaliana TDNA insertion lines  
DEFINITION Arabidopsis thaliana genomic clone SALK\_008070.43.05.x, DNA  
sequence.  
ACCESSION BH747013  
VERSION BH747013.1 GI:18960128  
KEYWORDS GSS.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 153)  
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadtrina,  
, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Predits, L., Shinn, P.,  
, Zimmerman, J. and Ecker, J.R.  
A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
Unpublished (2001)  
JOURNAL  
COMMENT Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: eckersalk.edu  
This is single pass sequence recovered from the left border of  
TDNA.  
Class: TDNA tagged.  
FEATURES  
source Location/Qualifiers  
1..153  
/organism="Arabidopsis thaliana"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_045100.51.10.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"  
BASE COUNT 37 a 35 c 37 g 49 t  
ORIGIN  
Query Match 8.7%; Score 40.4; DB 17; Length 158;  
Best Local Similarity 88.0%; Pred. No. 2.9;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_008070.43.05.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"  
BASE COUNT 47 a 37 c 33 g 36 t  
ORIGIN  
Query Match 8.7%; Score 40.4; DB 17; Length 153;  
Best Local Similarity 88.0%; Pred. No. 2.9;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 258 GATTGATGATATCTCCACTGACGTAAAGGATGACGACGACGACTA 307  
|||||  
Db 44 GATTGATGATATCTCCACTGACGTAAAGGATGACGACGACGACTA 93  
|||||  
RESULT 10  
BH748291/c 158 bp DNA linear GSS 27-FEB-2002  
LOCUS SALK\_045100.51.10 x Arabidopsis thaliana TDNA insertion lines  
DEFINITION Arabidopsis thaliana genomic clone SALK\_045100.51.10.x, DNA  
sequence.  
ACCESSION BH748291  
VERSION BH748291.1 GI:18961648  
KEYWORDS GSS.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 158)  
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadtrina,  
, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Predits, L., Shinn, P.,  
, Zimmerman, J. and Ecker, J.R.  
A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
Unpublished (2001)  
JOURNAL  
COMMENT Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: eckersalk.edu  
This is single pass sequence recovered from the left border of  
TDNA.  
Class: TDNA tagged.  
FEATURES  
source Location/Qualifiers  
1..158  
/organism="Arabidopsis thaliana"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_045100.51.10.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"  
BASE COUNT 37 a 35 c 37 g 49 t  
ORIGIN  
Query Match 8.7%; Score 40.4; DB 17; Length 158;  
Best Local Similarity 88.0%; Pred. No. 2.9;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAGGATGACGATCCACGACTA 307  
 |||||||  
 DB 110 GATTGATGATATCTCCACTGACGTAGGATGACGATCCACGACTA 61

RESULT 11  
 BH747357 165 bp DNA linear GSS 27-FEB-2002  
 LOCUS SALK\_016522.55.50.x Arabidopsis thaliana TDNA insertion lines  
 DEFINITION Arabidopsis thaliana genomic clone SALK\_016522.55.50.x, DNA  
 sequence.

ACCESSION BH747357  
 VERSION BH747357.1 GI:18960472  
 KEYWORDS GSS.  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana

REFERENCE  
 Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 Alonso,J.M., Leisbe,T.J., Barajas,P., Chen,H., Cheuk,R., Gadgilnab  
 'C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,  
 Zimmerman,J. and Ecker,J.R.  
 A Sequence-Indexed Library of Insertion Mutations in the  
 Arabidopsis Genome  
 Unpublished (2001)  
 CONTACT: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGNAL)  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu  
 This is single pass sequence recovered from the left border of  
 TDNA.

FEATURES  
 source  
 Location/Qualifiers  
 1..165  
 /organism="Arabidopsis thaliana"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_016522.55.50.x"  
 /note="lib-Arabidopsis thaliana TDNA insertion lines"  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)

BASE COUNT 45 a 43 c 39 g 38 t

ORIGIN

Query Match 8.7%; Score 40.4; DB 17; Length 165;  
 Best Local Similarity 88.0%; Pred. No. 2.9;  
 Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAGGATGACGATCCACGACTA 307  
 |||||||  
 DB 34 GATTGATGATATCTCCACTGACGTAGGATGACGATCCACGACTA 83

RESULT 12  
 BH746616 175 bp DNA linear GSS 27-FEB-2002  
 LOCUS SALK\_045268.54.50.x Arabidopsis thaliana TDNA insertion lines  
 DEFINITION Arabidopsis thaliana genomic clone SALK\_045268.54.50.x, DNA  
 sequence.

ACCESSION BH746616  
 VERSION BH746616.1 GI:18959731  
 KEYWORDS GSS.  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana

REFERENCE  
 Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 Alonso,J.M., Leisbe,T.J., Barajas,P., Chen,H., Cheuk,R., Gadgilnab  
 'C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,  
 Zimmerman,J. and Ecker,J.R.  
 A Sequence-Indexed Library of Insertion Mutations in the  
 Arabidopsis Genome  
 Unpublished (2001)  
 CONTACT: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGNAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu  
 This is single pass sequence recovered from the left border of  
 TDNA.

FEATURES  
 source  
 Location/Qualifiers  
 1..175  
 /organism="Arabidopsis thaliana"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_045268.54.50.x"  
 /note="lib-Arabidopsis thaliana TDNA insertion lines"  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)

BASE COUNT 54 a 43 c 40 g 38 t

ORIGIN

Query Match 8.7%; Score 40.4; DB 17; Length 175;  
 Best Local Similarity 88.0%; Pred. No. 3;  
 Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAGGATGACGATCCACGACTA 307  
 |||||||  
 DB 66 GATTGATGATATCTCCACTGACGTAGGATGACGATCCACGACTA 115

RESULT 13  
 BH802465 177 bp DNA linear GSS 25-APR-2002  
 LOCUS BH802465.1 y2 1008 - RescuedMu Grid 1 Zea mays genomic, DNA  
 DEFINITION

ACCESSION BH802465  
 VERSION BH802465.1 GI:20316614  
 KEYWORDS GSS.  
 SOURCE Zea mays.  
 ORGANISM Zea mays

REFERENCE  
 Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 177)  
 Walbot,V.  
 Maize genomic sequences found using engineered RescuedMu transposon  
 Unpublished (2001)  
 CONTACT: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Very probable ligation site found so sequence was trimmed.  
 post-ligation sequence submitted separately.  
 Plate: 1008026 row: 10  
 Class: transposon-tagged.  
 Location/Qualifiers

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source
1. .177
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1008 - RescueMu Grid 1"
/cisue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: leaf; Vector: RescueMu (engineered from
pInuScript backbone); Site_1: BamHI; Site_2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site www.zmhd.iastate.edu and follow the links for
'RescueMu.' Grid 1 was grown at Berkeley in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

BASE COUNT      39 a      38 c      47 g      53 t

ORIGIN
Query Match      8.7%; Score 40.4; DB 17; Length 177;
Best Local Similarity 88.0%; Pred. No. 3;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAAAGGATGACGATCCACGACTA 307
|||||
Db 118 GATTGATGATATCTCCACTGACGTAAAGGATGACGACAAATCCACTA 69

RESULT 14
BH752801      190 bp      DNA      linear      GSS 27-FEB-2002
LOCUS      SALK_019366.54.25.x Arabidopsis thaliana TDNA insertion lines
DEFINITION      Arabidopsis thaliana genomic clone SALK_019366.54.25.x. DNA
sequence.
ACCESSION      BH752801
VERSION      BH752801
KEYWORDS      GSS.
SOURCE      SALK_019366.54.25.x
ORGANISM      Arabidopsis thaliana
            thale cress.
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
            1 (bases 1 to 190)
            Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadgilnab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
            Zimmerman,J. and Ecker,J.R.
            A sequence-indexed library of Insertion Mutations in the
            Arabidopsis Genome
            Unpublished (2001)
            Contact: Joseph R. Ecker
            The Salk Institute Genomic Analysis Laboratory (SIGNAL)
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.

FEATURES
Class: TDNA tagged.
Location/Qualifiers
1. .190
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_019366.54.25.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was

```

```

directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna-protocols.html"

BASE COUNT      52 a      52 c      41 g      45 t

ORIGIN
Query Match      8.7%; Score 40.4; DB 17; Length 190;
Best Local Similarity 88.0%; Pred. No. 3;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAAAGGATGACGATCCACGACTA 307
|||||
Db 81 GATTGATGATATCTCCACTGACGTAAAGGATGACGACAAATCCACTA 130

RESULT 15
BH748289      193 bp      DNA      linear      GSS 27-FEB-2002
LOCUS      SALK_045097.54.25.x Arabidopsis thaliana TDNA insertion lines
DEFINITION      Arabidopsis thaliana genomic clone SALK_045097.54.25.x. DNA
sequence.
ACCESSION      BH748289
VERSION      BH748289.1 GI:18961643
KEYWORDS      GSS.
SOURCE      SALK_045097.54.25.x
ORGANISM      Arabidopsis thaliana
            thale cress.
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
            1 (bases 1 to 193)
            Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadgilnab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
            Zimmerman,J. and Ecker,J.R.
            A sequence-indexed library of Insertion Mutations in the
            Arabidopsis Genome
            Unpublished (2001)
            Contact: Joseph R. Ecker
            The Salk Institute Genomic Analysis Laboratory (SIGNAL)
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.

FEATURES
Class: TDNA tagged.
Location/Qualifiers
1. .193
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_045097.54.25.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
            directly sequenced to determine the genomic sequence at
            the site of insertion. Details of the protocols used can
            be found at http://signal.salk.edu/tdna-protocols.html"

BASE COUNT      61 a      48 c      43 g      41 t

ORIGIN
Query Match      8.7%; Score 40.4; DB 17; Length 193;
Best Local Similarity 88.0%; Pred. No. 3;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGATATCTCCACTGACGTAAAGGATGACGATCCACGACTA 307
|||||
Db 84 GATTGATGATATCTCCACTGACGTAAAGGATGACGACAAATCCACTA 133

Search completed: April 14, 2003, 10:25:44
Job time : 1075.87 secs

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GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 04:10:42 ; Search time 1713.81 Seconds

(without alignments)  
10186.783 Million cell updates/sec

Title: US-09-963-803-22

Perfect score: 600

Sequence: 1 aagcttgcatgcctgcagca.....cacacaactagagatcc 600

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_da: \*  
2: gb\_htg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vi: \*  
15: em\_ba: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_mu: \*  
20: em\_om: \*  
21: em\_or: \*  
22: em\_ov: \*  
23: em\_ph: \*  
24: em\_pl: \*  
25: em\_pi: \*  
26: em\_ro: \*  
27: em\_sts: \*  
28: em\_un: \*  
29: em\_vi: \*  
30: em\_htg\_hum: \*  
31: em\_htg\_inv: \*  
32: em\_htg\_mus: \*  
33: em\_htg\_other: \*  
34: em\_htg\_pln: \*  
35: em\_htg\_rtd: \*  
36: em\_htg\_mam: \*  
37: em\_htg\_vrt: \*  
38: em\_sy: \*  
39: em\_htgo\_hum: \*  
40: em\_htgo\_mus: \*  
41: em\_htgo\_other: \*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID       | Description        |
|------------|-------|-------------|--------|----|----------|--------------------|
| 1          | 600   | 100.0       | 600    | 6  | AX036756 | AX036756 Sequence  |
| 2          | 587   | 97.8        | 9285   | 6  | AX093047 | AX093047 Sequence  |
| 3          | 587   | 97.8        | 15077  | 6  | AX093052 | AX093052 Sequence  |
| 4          | 373.6 | 62.3        | 462    | 6  | AX036754 | AX036754 Sequence  |
| 5          | 312.2 | 52.0        | 604    | 6  | AX036757 | AX036757 Sequence  |
| 6          | 304.6 | 50.8        | 393    | 6  | AX036753 | AX036753 Sequence  |
| 7          | 281.4 | 46.9        | 541    | 6  | AX036758 | AX036758 Sequence  |
| 8          | 234.2 | 39.0        | 392    | 6  | AX036755 | AX036755 Sequence  |
| 9          | 212.4 | 35.4        | 317    | 6  | AX036737 | AX036737 Sequence  |
| 10         | 212.4 | 35.4        | 472    | 6  | AX036738 | AX036738 Sequence  |
| 11         | 200.4 | 33.4        | 348    | 6  | AX036739 | AX036739 Sequence  |
| 12         | 152.8 | 25.5        | 371    | 6  | AX036739 | AX036739 Sequence  |
| 13         | 140.8 | 23.5        | 301    | 6  | AX036741 | AX036741 Sequence  |
| 14         | 140.8 | 23.5        | 398    | 6  | AX036740 | AX036740 Sequence  |
| 15         | 120.6 | 20.1        | 515    | 6  | AX036736 | AX036736 Sequence  |
| 16         | 120.6 | 20.1        | 515    | 6  | AX088388 | AX088388 Sequence  |
| 17         | 120.6 | 20.1        | 532    | 6  | AX202413 | AX202413 Sequence  |
| 18         | 120.6 | 20.1        | 838    | 6  | AX014764 | AX014764 Sequence  |
| 19         | 120.6 | 20.1        | 853    | 6  | AX088389 | AX088389 Sequence  |
| 20         | 120.6 | 20.1        | 1036   | 6  | AX014765 | AX014765 Sequence  |
| 21         | 120.6 | 20.1        | 8158   | 14 | CV020341 | U20341 Cassava vel |
| 22         | 120.6 | 20.1        | 8159   | 14 | CV059751 | U59751 Cassava vel |
| 23         | 120.6 | 20.1        | 8340   | 6  | AX329231 | AX329231 Sequence  |
| 24         | 120.6 | 20.1        | 8340   | 6  | AX338536 | AX338536 Sequence  |
| 25         | 120.6 | 20.1        | 12241  | 6  | AX412168 | AX412168 Sequence  |
| 26         | 115.8 | 19.3        | 593    | 6  | AX088390 | AX088390 Sequence  |
| 27         | 115.8 | 19.3        | 857    | 6  | AX088391 | AX088391 Sequence  |
| 28         | 115.8 | 19.3        | 931    | 6  | AX088392 | AX088392 Sequence  |
| 29         | 115.4 | 19.2        | 931    | 6  | AX088393 | AX088393 Sequence  |
| 30         | 115.4 | 19.2        | 931    | 6  | AX088393 | AX088393 Sequence  |
| 31         | 81.4  | 13.6        | 7489   | 14 | CYMWCG   | X52938 Commelina Y |
| 32         | 80    | 13.3        | 243    | 6  | AX036735 | AX036735 Sequence  |
| 33         | 75.4  | 12.6        | 392    | 6  | AX036755 | AX036755 Sequence  |
| 34         | 69.6  | 11.6        | 79     | 6  | AX036611 | AX036611 Sequence  |
| 35         | 69.6  | 11.6        | 79     | 6  | AX036748 | AX036748 Sequence  |
| 36         | 69.6  | 11.6        | 296    | 6  | AX036603 | AX036603 Sequence  |
| 37         | 69    | 11.5        | 259    | 6  | AX036616 | AX036616 Sequence  |
| 38         | 62    | 10.3        | 62     | 6  | AX036744 | AX036744 Sequence  |
| 39         | 60    | 10.0        | 60     | 6  | AX036743 | AX036743 Sequence  |
| 40         | 60    | 10.0        | 63     | 6  | AX036746 | AX036746 Sequence  |
| 41         | 58    | 9.7         | 80     | 6  | AX103782 | AX103782 Sequence  |
| 42         | 58    | 9.7         | 236    | 6  | AX103783 | AX103783 Sequence  |
| 43         | 58    | 9.7         | 299    | 6  | AX103784 | AX103784 Sequence  |
| 44         | 58    | 9.7         | 332    | 6  | AX103755 | AX103755 Sequence  |
| 45         | 58    | 9.7         | 472    | 6  | AX103753 | AX103753 Sequence  |

#### ALIGNMENTS

RESULT 1  
AX036756  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

AX036756  
Sequence 22 from Patent WO0058465.  
AX036756  
AX036756.1 GI:11226265  
synthetic construct.  
artificial sequences.  
1 (bases 1 to 600)  
Rance, I., Theisen, M. and Gruber, V.  
Chimeric expression promoters originating from commelina yellow  
mottle virus and cassava vein mosaic virus  
Patent: WO 0058465-A 22 OCT-2000.

600 bp. DNA 1linear PAT 16-NOV-2000

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MERISEUM THERAPEUTICS (FR) ; RANGE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
FEATURES      Location/Qualifiers
SOURCE      1. .600

```

promoter  
BASE COUNT  
ORIGIN

|                       |                 |                   |           |             |
|-----------------------|-----------------|-------------------|-----------|-------------|
| Query Match           | 100.0%;         | Score 600;        | DB 6;     | Length 600; |
| Best Local Similarity | 100.0%;         | Pred. NO. 7e-154; |           |             |
| Matches 600;          | Conservative 0; | Mismatches 0;     | Indels 0; | Gaps 0;     |

|    |     |   |     |
|----|-----|---|-----|
| QY | 1   | AAATTCGATCGCGACACACACAGTAAATCCGCGCTATCAATACATCAACAGTACTGA       | 60  |
| Db | 1   | AAGCTTGATCCCTCGACACACTAGTATCCGCGCTATCAATACATCAACAGTACTGA        | 60  |
| QY | 61  | GGAGATGAATAGCTAGGCCATGACACTCTGTGGCGAATATTGAAGACGTAAAGCACTAGCAG  | 120 |
| Db | 61  | GGAGATGAATAGCTAGGCCATGACACTCTGTGGGAATATTGAAGAGGTAAAGCACTAGCAG   | 120 |
| QY | 121 | AACCAATGAAAAAGAGAAACATTAAGTCCGTGATTGTGAAAAGAGACATAGAGCACACATGTA | 180 |
| Db | 121 | AACCAATGAAAAAGAAACAAATTAAGGTCGGTGTGTAAGAGACATAGAGGACACATGTA     | 180 |
| QY | 181 | AGGTGAAATATGTAAAGGCGGAAACATAACCTATATGATTTGTAAATTTGGTTACGACTACT  | 240 |
| Db | 181 | AGGTGAAATATGTAAAGGCGGAAACATAACCTTATATGATTTGTAAATTTGGTTACGACTACT | 240 |
| QY | 241 | GATTGATGCTGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATGACGCATGCC   | 300 |
| Db | 241 | GATTGATGCTGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATGACGCATGCC   | 300 |
| QY | 301 | ACGACTAGTATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATG     | 360 |
| Db | 301 | ACGACTAGTATTGATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATG     | 360 |
| QY | 361 | ACGCATGCGACAGACAGTATGATGTGATATCAAGATTGATGTATATCTCCACTGACG       | 420 |
| Db | 361 | ACGCATGCGACAGACAGTATGATGTGATATCAAGATTGATGTATATCTCCACTGACG       | 420 |
| QY | 421 | TAAAGGATGACGCATGATCCACGACTAGTATGATGATATCAAGATTGATGTATATCT       | 480 |
| Db | 421 | TAAAGGATGACGCATGATCCACGACTAGTATGATGATATCAAGATTGATGTATATCT       | 480 |
| QY | 481 | CCACTGACGTAAAGGATGACGCATGCCAGCTTACCCGGTATGCCGGTTCCCAAGCTTTAT    | 540 |
| Db | 481 | CCACTGACGTAAAGGATGACGCATGCCAGCTTACCCGGTATGCCGGTTCCCAAGCTTTAT    | 540 |
| QY | 541 | TTTCCTTATTTAAGCACTGTGTAGTAGCTTAGAAAAACCAACCAACCACTTAGAGATGCC    | 600 |
| Db | 541 | TTTCCTTATTTAAGCACTGTGTAGTAGCTTAGAAAAACCAACCAACCACTTAGAGATGCC    | 600 |

|            |                                    |             |        |
|------------|------------------------------------|-------------|--------|
| RESULT 2   |                                    |             |        |
| AX093047   |                                    |             |        |
| LOCUS      | AX093047                           | 9285 bp     | DNA    |
| DEFINITION | Sequence 52 from Patent WO0118192. |             | linear |
| ACCESSION  | AX093047                           |             |        |
| VERSION    | AX093047.1                         | GI:13509522 |        |

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source      1. .9285      /organism="synthetic construct"  
            /db_xref="taxon:32630"  
            /note="PMRT136"  
misc_feature 1
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|            |  |        |        |        |
|------------|--|--------|--------|--------|
| BASE COUNT | 2440 a   | 2252 c | 2506 g | 2087 t |
| ORIGIN     | /note="PMR1336 results from the insertion into PMR1196 of the promoter MP1165 isolated from plasmid PMR1332 as described in PCT patent application PCT/IB00/00370" |        |        |        |

|                       |              |            |            |              |
|-----------------------|--------------|------------|------------|--------------|
| Query Match           | 97.8%        | Score 587; | DB 6;      | Length 9285; |
| Best Local Similarity | 100.0%       | Pred. NO.  | 2.3e-150;  |              |
| Matches 587;          | Conservative | 0;         | Mismatches | 0;           |
|                       |              |            | Indels     | 0;           |
|                       |              |            | Gaps       | 0;           |

|    |      |   |      |
|----|------|---|------|
| QY | 10   | TGCTCGACGACCTAGTATCCGCCCTCATCATGACATCATTAACAGTACTGAGGAGATGAA    | 69   |
| Db | 5799 | TGCTCGACGACCTAGTATCCGCCCTCATCATGACATCATTAACAGTACTGAGGAGATGAA    | 5858 |
| QY | 70   | TAGCTAGCCATGACACTCTGTGCGAATTTATMAACGTAAGCACTGACGACAAACAATGAA    | 129  |
| Db | 5859 | TAGCTAGCCATGACACTCTGTGCGAATTTATMAACGTAAGCACTGACGACAAACAATGAA    | 5918 |
| QY | 130  | AAGAAGAAGATTAAGGTGCGGTGATTGTGAAAGACACATAGACACACATGTAAGTGGAAA    | 189  |
| Db | 5919 | AAGAAGAAGATTAAGGTGCGGTGATTGTGAAAGACACATAGACACACATGTAAGTGGAAA    | 5978 |
| QY | 190  | ATGTAAAGGGCGGAAAGTAACCTTATGCACTTTGTATATTGGTTAGACACTAGATTGATGT   | 249  |
| Db | 5979 | ATGTAAAGGGCGGAAAGTAACCTTATGCACTTTGTATATTGGTTAGACACTAGATTGATGT   | 6038 |
| QY | 250  | GATATCAAGATTGATGTGATATCTCCACTGACGTAAGGGATGAGCGCATGCCACGACTAGT   | 309  |
| Db | 6039 | GATATCAAGATTGATGTGATATCTCCACTGACGTAAGGGATGAGCGCATGCCACGACTAGT   | 6098 |
| QY | 310  | GATTGATGTGATATTCACAGATTGATGTGATATCTCCACTGACGTAAGGGATGAGCGCATGCC | 369  |
| Db | 6099 | GATTGATGTGATATTCACAGATTGATGTGATATCTCCACTGACGTAAGGGATGAGCGCATGCC | 6158 |
| QY | 370  | ACGACTACTGATTTGATGATATCAAGTTGATGATATCTCCACTGACGTAAGGGATG        | 429  |
| Db | 6159 | ACGACTACTGATTTGATGATATCAAGTTGATGATATCTCCACTGACGTAAGGGATG        | 6218 |
| QY | 430  | ACGATGCGCACGACAGTATGATTTGATGTGATATCAAGATTGATGTGATATCTCCACTGACG  | 489  |
| Db | 6219 | ACGATGCGCACGACAGTATGATTTGATGTGATATCAAGATTGATGTGATATCTCCACTGACG  | 6278 |
| QY | 490  | TAAAGGATGACGATGCCACGTTACCCGGTATGCCGGTTGCCAAGCTTATTTCTTAATT      | 549  |
| Db | 6279 | TAAAGGATGACGATGCCACGTTACCCGGTATGCCGGTTGCCAAGCTTATTTCTTAATT      | 6338 |
| QY | 550  | TAAGCATCTGTGTAGTACCTTAGAAAAACAACAACAACCAACTAAGG                 | 596  |
| Db | 6339 | TAAGCATCTGTGTAGTACCTTAGAAAAACAACAACAACAACCTAAGG                 | 6385 |

| RESULT 3   | AX093052   | LOCUS                              | AX093052 | Sequence 57 from Patent WO0118192. | 15077 bp | DNA | Linear | PAT 30-MAR-2001 |
|------------|------------|------------------------------------|----------|------------------------------------|----------|-----|--------|-----------------|
| DEFINITION | AX093052   | Sequence 57 from Patent WO0118192. |          |                                    |          |     |        |                 |
| ACCESSION  | AX093052   | AX093052.1                         |          |                                    |          |     |        |                 |
| VERSION    | AX093052.1 | GI:13509527                        |          |                                    |          |     |        |                 |

|           |  |
|-----------|--|
| ORGANISM  | synthetic construct  |
| REFERENCE | artificial sequences.  |
| AUTHORS   | 1. (bases 1 to 9285).  |
| TITLE     | Gruber, V. and Cameau, D.  |
| JOURNAL   | Synthetic vectors, transgenic plants containing them, and methods for obtaining them |
| FEATURES  | Patent: WO 0118192-A 52 15-MAR-2001;   |
|           | MERISTEM THERAPEUTICS (FR)   |
|           | Location/Qualifiers  |

| ORGANISM  | synthetic construct<br>artificial sequence.   |
|-----------|---|
| REFERENCE | 1 (bases 1 to 15077).   |
| AUTHORS   | Gruber, V. and Cemeau, D.   |
| TITLE     | Synthetic vectors, transgenic plants containing them, and methods<br>for obtaining them |
| JOURNAL   | Patent: WO 0118192-A 57 15-MAR-2001:  |
| FEATURES  | MERISTEM THERAPEUTICS (FR)<br>location/Qualifiers                                       |

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source 1. .15077
        /organism="synthetic construct"
        /db_xref="taxon:32630"
misc_feature 1
             /note="pMR1342 results from the replacement of the
             expression cassette ep35S-gus-polyA35S from pMR1335 by
             the expression cassette L5-gus-polyA35S isolated from
             pMR1336"
BASE COUNT 3672 a 3892 c 4225 g 3288 t
ORIGIN
Query Match 97.8%; Score 587; DB 6; Length 15077;
Best Local Similarity 100.0%; Pred. No. 2.2e-150;
Matches 587; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 TGCCTGACGACCTAGTATCCGCGCTCATATGACATCATACAGTACTAGAGATGAA 69
    |||||||
DB 6838 TGCCTGACGACCTAGTATCCGCGCTCATATGACATCATACAGTACTAGAGATGAA 6897
    |||||||
QY 70 TAGCTAGCCATGACACCTGTGGAAATTTGAAGAGCTAGACCTGACGCAACAATGAA 129
    |||||||
DB 6898 TAGCTAGCCATGACACCTGTGGAAATTTGAAGAGCTAGACCTGACGCAACAATGAA 6957
    |||||||
QY 130 AAGAAGATAGTAAAGTGTGATTTGTAAGAGACATAGAGACACATGTAAAGTGAAA 189
    |||||||
DB 6958 AAGAAGATAGTAAAGTGTGATTTGTAAGAGACATAGAGACACATGTAAAGTGAAA 7017
    |||||||
QY 190 ATGTAAAGGCGGAAAGTAACTTATGCTATTTGTTACGACTAGTATGATGT 249
    |||||||
DB 7018 ATGTAAAGGCGGAAAGTAACTTATGCTATTTGTTACGACTAGTATGATGT 7077
    |||||||
QY 250 GATATCAAGTTGATGTGATATCTCCACGTAAGGAAATGACGATGCGACAGT 309
    |||||||
DB 7078 GATATCAAGTTGATGTGATATCTCCACGTAAGGAAATGACGATGCGACAGT 7137
    |||||||
QY 310 GATTGATGATATCAAGATTTGATATCTCCACTGACGTAAGGATAGCGATGCC 369
    |||||||
DB 7138 GATTGATGATATCAAGATTTGATATCTCCACTGACGTAAGGATAGCGATGCC 7197
    |||||||
QY 370 ACAGCTAGTATGATGTGATATCAAGATTTGATATCTCCACTGACGTAAGGATG 429
    |||||||
DB 7198 ACAGCTAGTATGATGTGATATCAAGATTTGATATCTCCACTGACGTAAGGATG 7257
    |||||||
QY 430 ACCGATGCCAGCTAGTATGATATCAAGATTTGATATCTCCACTGACGTAAGG 489
    |||||||
DB 7258 ACCGATGCCAGCTAGTATGATATCAAGATTTGATATCTCCACTGACGTAAGG 7317
    |||||||
QY 490 TAAGGATGACGATGCGATACCGGATGCGGTTCCCAAGCTTATTTCCCTATT 549
    |||||||
DB 7318 TAAGGATGACGATGCGATACCGGATGCGGTTCCCAAGCTTATTTCCCTATT 7377
    |||||||
QY 550 TAAGCACTTGTAGTAGCTTAAAGAAACAACAACAACACCTAGAGG 596
    |||||||
DB 7378 TAAGCACTTGTAGTAGCTTAAAGAAACAACAACAACACCTAGAGG 7424
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RESULT 4
AX036754 462 bp DNA linear PAT 16-NOV-2000
LOCUS Sequence 20 from Patent WO0058485.
DEFINITION AX036754
ACCESSION AX036754
VERSION AX036754.1 GI:11226263
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE
1 (bases 1 to 462)
AUTHORS
Rance, I., Theisen, M. and Gruber, V.
TITLE
Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
PATENT: WO 0058485-A 20 05-OCT-2000;
JOURNAL
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
```

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FEATURES ; GRUBER VERONIQUE (FR)
source 1. .462
        /organism="synthetic construct"
        /db_xref="taxon:32630"
        /note="promoter Mpr1163"
promoter 1. .462
BASE COUNT 148 a 87 c 111 g 116 t
ORIGIN
Query Match 62.3%; Score 373.6; DB 6; Length 462;
Best Local Similarity 95.3%; Pred. No. 8.9e-92;
Matches 385; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 1 AAGCTTGATGCTGCGACGCTAGTATCCCGCTGATCATATGATATATACAGTACTGA 60
    |||||||
DB 1 AAGCTTGATGCTGCGACGCTAGTATCCCGCTGATCATATGATATATACAGTACTGA 60
    |||||||
QY 61 GGAGATGAATAGCTAGGACACCTGTGCGAATTTGAAGACGTAAGCACTAGACGAC 120
    |||||||
DB 61 GGAGATGAATAGCTAGGACACCTGTGCGAATTTGAAGACGTAAGCACTAGACGAC 120
    |||||||
QY 121 AACATGAAAAAAGAAATAGGTGCGTATTTGTGAAAGACATAGAGACATGTA 180
    |||||||
DB 121 AACATGAAAAAAGAAATAGGTGCGTATTTGTGAAAGACATAGAGACATGTA 180
    |||||||
QY 181 AGGTGAAAAATGTAAGGCGGAAAGTAACTTATGCAATTTGTAATTTGTTACGACTAGT 240
    |||||||
DB 181 AGGTGAAAAATGTAAGGCGGAAAGTAACTTATGCAATTTGTAATTTGTTACGACTAGT 240
    |||||||
QY 241 GATTGATGATATCAAGATTTGATATCTCCACTGACGTAAGGATAGCGATGCC 300
    |||||||
DB 241 GATTGATGATATCAAGATTTGATATCTCCACTGACGTAAGGATAGCGATGCC 300
    |||||||
QY 301 ACAGCTAGTATGATGTGATATCAAGATTTGATATCTCCACTGACGTAAGGATG 360
    |||||||
DB 301 ACAGCTAGTATGATGTGATATCAAGATTTGATATCTCCACTGACGTAAGGATG 360
    |||||||
QY 361 ACCGATGCCAGCTAGTATGATATCAAGATTTGATATCTCCACTGACGTAAGGATG 404
    |||||||
DB 361 ACCGATGCCAGCTAGTATGATATCAAGATTTGATATCTCCACTGACGTAAGGATG 404
    |||||||
RESULT 5
AX036757 604 bp DNA linear PAT 16-NOV-2000
LOCUS Sequence 23 from Patent WO0058485.
DEFINITION AX036757
ACCESSION AX036757
VERSION AX036757.1 GI:11226266
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE
1 (bases 1 to 604)
AUTHORS
Rance, I., Theisen, M. and Gruber, V.
TITLE
Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
PATENT: WO 0058485-A 23 05-OCT-2000;
JOURNAL
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
FEATURES
source 1. .604
        /organism="synthetic construct"
        /db_xref="taxon:32630"
        /note="promoter Mpr1167"
promoter 1. .604
BASE COUNT 186 a 116 c 145 g 157 t
ORIGIN
Query Match 52.0%; Score 312.2; DB 6; Length 604;
Best Local Similarity 84.5%; Pred. No. 6.1e-75;
Matches 442; Conservative 0; Mismatches 3; Indels 78; Gaps 5;
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|                           |  |                    |  |                 |
|---------------------------|--|--------------------|--|-----------------|
| Oy                        |  | 78                 | CATGACACTCTGTGGGATTATTGAAGACGTAAAGCACTACGCACAACAATTAAGAAGAACAA   | 137             |
| Dd                        |  | 160                | CATGCCACTCTGTGGGAATTATTTAAGACGTAAAGCACTACGCACAACAATTAAGAAGAACAA  | 219             |
| Oy                        |  | 138                | GATAAGTCGCGTGATTTTGAAGAGACATATAGAGCACATGTAAAGTGGAAAAATTGAAG      | 197             |
| Dd                        |  | 220                | GATTAAAGTCGCGTGATTTG-T- AAGAGACATATAGAGCACATGTAAAGTGGAAAAATTGAAG | 278             |
| Oy                        |  | 198                | GGGGAAGTAAACCTTATGSCATTTTGTAAATTGGTTTAGCAGCTAGTATGTATGATATCAA    | 257             |
| Dd                        |  | 279                | GGGGAAGTAAACCTTATGSCATTTTGTAAATTGGTTTAGCAGCTAGTATGTATGATATCAA    | 314             |
| Oy                        |  | 258                | GATTATGTATGTATCTCCACGTACGCTAAAGGATAGCCATGCCAGCTAGTATGATG         | 317             |
| Dd                        |  | 315                | - - - - - CTAGTATTTGATG  | 327             |
| Oy                        |  | 318                | TGATATCAAGATTGATGTATCTCCACGTACGCTAAAGGATAGCCATGCCAGCTAG          | 377             |
| Dd                        |  | 328                | TGATATCAAGATTGATGTATCTCCACGTACGCTAAAGGATAGCCATGCCAGCTAG          | 385             |
| Oy                        |  | 378                | TGATTGATGTATATCAAGATTGATGTATCTCCACGTACGCTAAAGGATAGCATGC          | 437             |
| Dd                        |  | 386                | TGATTGATGTATATCAAGATTGATGTATCTCCACGTACGCTAAAGGATAGCATGC          | 445             |
| Oy                        |  | 438                | CACGACATGATGTATGTATATCAAGATTGATGTATCTCCACGTACGCTAAAGGAT          | 497             |
| Dd                        |  | 446                | CAC -- CTAGTATGTATGTATGTATATCAAGATTGATGTATCTCCACGTACGCTAAAGGAT   | 503             |
| Oy                        |  | 498                | GACGATGCGCAGTTATACCCTGATACCCGGTTCCCAAGCTTATTTCTTATTGAAGCACT      | 557             |
| Dd                        |  | 504                | GACGATGCGCAGTTATACCCTGATACCCGGTTCCCAAGCTTATTTCTTATTGAAGCACT      | 561             |
| Oy                        |  | 558                | TGTGTAGTAGCTTTGAAAACCAACCAACAACCTAGAGATCC                        | 600             |
| Dd                        |  | 562                | TGTGTAGTAGCTTTGAAAACCAACCAACAACCTAGAGATCC                        | 604             |
| RESULT 6                  |  |                    |  |                 |
| AX036753                  |  |                    |  |                 |
| LOCUS                     | AX036753   | 393 bp             | DNA  | Linear          |
| DEFINITION                | Sequence 19 from Patent WO0058485.   |                    |  | PAT 16-NOV-2000 |
| ACCESSION                 | AX036753   |                    |  |                 |
| VERSION                   | AX036753.1   | GI:11226262        |  |                 |
| KEYWORDS                  | .  |                    |  |                 |
| SOURCE                    | synthetic construct.   |                    |  |                 |
| ORGANISM                  | artificial sequences.  |                    |  |                 |
| REFERENCE                 | 1 (bases 1 to 393)   |                    |  |                 |
| AUTHORS                   | Rance,I., Theisen,M. and Gruber,V.   |                    |  |                 |
| TITLE                     | Chimeric expression promoters originating from commelina yellow mottle virus and cassava vein mosaic |                    |  |                 |
| JOURNAL                   | Patent: WO 0058485-A 19 05-OCT-2000:   |                    |  |                 |
|                           | MELISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)                                  |                    |  |                 |
| FEATURES                  | ; GRUBER VERONIQUE (FR)  |                    |  |                 |
| source                    | Location/Qualifiers  |                    |  |                 |
|                           | 1..393   |                    |  |                 |
|                           | /organism="synthetic construct"  |                    |  |                 |
|                           | /db_xref="taxon:32630"   |                    |  |                 |
|                           | /note="promoter MPril62"   |                    |  |                 |
| BASE COUNT                | 128 a 75 c 93 g 97 t   |                    |  |                 |
| ORIGIN                    |  |                    |  |                 |
| Query Match               | 50.8%;   | Score 304.6;       | DB 6;  | Length 393;     |
| Best Local Similarity     | 94.3%;   | Pred. No. 7.6e-73; |  |                 |
| Matches 316; Conservative | 0;   | Mismatches 19;     | Indels 0;  | Gaps 0;         |
| Oy                        | 1 AAGCTTGATGCGCTCACACACTAGTATCCGCGGTATCAATGACATCATCAGTACTGA  | 60                 |  |                 |
| Dd                        | 1 AAGCTTGATGCGCTCACACACTAGTATCCGCCGTATCAATGACATCATCAGTACTGA  | 60                 |  |                 |
| Oy                        | 61 GGAGATGATAGCTAGCCATGACACTCTGTGGGAATTATTTGAAGACGTAAAGCACTGACGAC                                    | 120                |  |                 |

[illegible]



RESULT 8  
AX036755  
LOCUS AX036755 392 bp DNA linear PAT 16-NOV-2000  
DEFINITION Sequence 21 from Patent W0058485.  
ACCESSION AX036755  
VERSION AX036755.1 GI:11226264  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM  
REFERENCE  
AUTHORS 1 (bases 1 to 392)  
Rance, I., Theisen, M. and Gruber, V.  
TITLE ChimERIC expression promoters originating from commelina yellow  
mottle virus and cassava vein mosaic virus  
JOURNAL Patent: WO 0058485-A 21 05-OCT-2000;  
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)  
; GRUBER VERONIQUE (FR)  
LOCATION/Qualifiers  
source 1..392  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="promoter MP11164"  
Promoter 1..392  
BASE COUNT 127 a 80 c 87 g 98 t  
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Query Match 39.0%; Score 234.2; DB 6; Length 392;  
Best Local Similarity 96.8%; Pred. No. 1.5e-53;  
Matches 239; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
QY 1 AAGCTGATGCTCGACACTAGTATCCGCCGTCATCAATAGACATCATCTACAGTACGA 60  
DB 1 AAGCTGATGCTCGACACTAGTATCCGCCGTCATCAATAGACATCATCTACAGTACGA 60  
QY 61 GGAGATGATAGTACGACACTCTGTGCGAATATTGAAGACGTAAAGCAGTACGAC 120  
DB 61 GGAGATGATAGTACGACACTCTGTGCGAATATTGAAGACGTAAAGCAGTACGAC 120  
QY 121 AACAAAGAAAGAAAGATAGGTGCGTGTGTAAGAGACATAGAGACATGTA 180  
DB 121 AACAAAGAAAGAAAGATAGGTGCGTGTGTAAGAGACATAGAGACATGTA 180  
QY 181 AGGTGAAAAATGTAAAGGCGGAAAGTAACTTATTCATTGTTGTTACGACTAGT 240  
DB 181 AGGTGAAAAATGTAAAGGCGGAAAGTAACTTATTCATTGTTGTTACGACTAGT 240  
QY 241 GATTGAT 247  
DB 241 GATTGAT 247  
RESULT 9  
AX036737  
LOCUS AX036737 317 bp DNA linear PAT 16-NOV-2000  
DEFINITION Sequence 3 from Patent W00058485.  
ACCESSION AX036737  
VERSION AX036737.1 GI:11226246  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM  
REFERENCE  
AUTHORS 1 (bases 1 to 317)  
Rance, I., Theisen, M. and Gruber, V.  
TITLE ChimERIC expression promoters originating from commelina yellow  
mottle virus and cassava vein mosaic virus  
JOURNAL Patent: WO 0058485-A 3 05-OCT-2000;  
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)  
; GRUBER VERONIQUE (FR)  
LOCATION/Qualifiers  
source 1..317  
/organism="synthetic construct"  
/db\_xref="taxon:32630"

/note="promoter MP11164"  
Promoter 1..317  
BASE COUNT 107 a 61 c 74 g 75 t  
ORIGIN  
Query Match 35.4%; Score 212.4; DB 6; Length 317;  
Best Local Similarity 99.5%; Pred. No. 1.5e-47;  
Matches 213; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 20 ACTAGATCCGCCGTCATCAATGACATCATCAGTACTGAGAGATGATAGTACCA 79  
DB 18 ACTAGATCCGCCGTCATCAATGACATCATCAGTACTGAGAGATGATAGTACCA 77  
QY 80 TGACACTCTGTGCGAATATTGAAGACGTAAAGCAGTACGACGACAAATGAAAAGAA 139  
DB 78 TGACACTCTGTGCGAATATTGAAGACGTAAAGCAGTACGACGACAAATGAAAAGAA 137  
QY 140 TAAAGTCGATGTTGTAAGAGACATAGAGACATGTAAAGTGGAATGTAAAGGC 199  
DB 138 TAAAGTCGATGTTGTAAGAGACATAGAGACATGTAAAGTGGAATGTAAAGGC 197  
QY 200 GGAAGTAACCTTATGCAATTTGTAATTTGTTAC 233  
DB 198 GGAAGTAACCTTATGCAATTTGTAATTTGTTAC 231  
RESULT 10  
AX036759  
LOCUS AX036759 472 bp DNA linear PAT 16-NOV-2000  
DEFINITION Sequence 25 from Patent W00058485.  
ACCESSION AX036759  
VERSION AX036759.1 GI:11226268  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM  
REFERENCE  
AUTHORS 1 (bases 1 to 472)  
Rance, I., Theisen, M. and Gruber, V.  
TITLE ChimERIC expression promoters originating from commelina yellow  
mottle virus and cassava vein mosaic virus  
JOURNAL Patent: WO 0058485-A 25 05-OCT-2000;  
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)  
; GRUBER VERONIQUE (FR)  
LOCATION/Qualifiers  
source 1..472  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="promoter MP11169"  
Promoter 1..472  
BASE COUNT 149 a 92 c 112 g 119 t  
ORIGIN  
Query Match 35.4%; Score 212.4; DB 6; Length 472;  
Best Local Similarity 91.5%; Pred. No. 1.5e-47;  
Matches 236; Conservative 0; Mismatches 21; Indels 1; Gaps 1;  
QY 78 CATGACACTCTGTGCGAATATTGAAGACGTAAAGCAGTACGACAAATGAAAAGAA 137  
DB 160 CATGACACTCTGTGCGAATATTGAAGACGTAAAGCAGTACGACAAATGAAAAGAA 219  
QY 138 GATAAGTCGCTGATTTGTGAAGAGACATAGAGACATGTAAGGTGGAATGTAAAG 197  
DB 220 GATAAGTCGCTGATTTGTG-AAGAGACATAGAGACATGTAAGGTGGAATGTAAAG 278  
QY 198 GCGAAAGTAACTTATGATTTGTAATTTGTTACGACGTGATGATGATGATATCAA 257  
DB 279 GCGAAAGTAACTTATGATTTGTAATTTGTTACGACGTGATGATGATGATATCAA 338  
QY 258 GATTGATGTGATATCTCACTGACGTAAAGGATGACGACGACGACTAGTATGATG 317  
DB 339 GATTGATGTGATATCTCACTGACGTAAAGGATGACGACGACGACTAGTATGATG 398  
QY 318 TGATATCAAGATTGATGT 335



artificial sequences.  
1 (bases 1 to 398)

**AUTHORS** Rance, I., Theisen, M. and Gruber, Y.  
**TITLE** Chimeric expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus  
**JOURNAL** Patent: WO 0058485-A 6 05-OCT-2000;  
MEISTHEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)  
\* GROUPED VERBOTEN (FR)

|            |       |      |      |
|------------|-------|------|------|
| promoter   | 1.    | .398 |      |
| BASE COUNT | 128 a | 80 c | 93 g |
| ORIGIN     |       |      | 97 t |

|            |                                   |
|------------|-----------------------------------|
| RESULT     | 15                                |
| LOCUS      | AX036736                          |
| DEFINITION | Sequence 2 from Patent WO0058485. |
| ACCESSION  | AX036736                          |
| VERSION    | AX036736.1                        |
| KEYWORDS   | GI:1126245                        |
|            |                                   |
|            | 515 bp                            |
|            | DNA                               |
|            | linear                            |
|            | PAT 16-NOV-2000                   |

|                       |                |                   |          |            |
|-----------------------|----------------|-------------------|----------|------------|
| Query Match           | 20.1%          | Score 120.6       | DB 6     | Length 515 |
| Best Local Similarity | 93.3%          | Score No. 2.2e-22 |          |            |
| Matches 126           | Conservative 0 | Mismatches 9      | Indels 0 | Gaps 0     |

|    |     |             |      |     |
|----|-----|-------------|------|-----|
| QY | 213 | ATGCATTGTAA | TTT  | 227 |
|    |     |             |      |     |
| Db | 336 | ATCACAAAGGA | ATCT | 350 |

Search completed: April 14, 2003, 09:29:40  
Job time : 1728.81 secs



GenCore version 5.1.4\_p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 04:03:41 ; Search time 193.814 Seconds  
(without alignments)  
6971.612 Million cell updates/sec

Title: US-09-963-803-22

Perfect score: 600

Sequence: 1 aaagcttgatgctgctgacga.....cacacaacctaagatgcc 600

Scoring table: IDENTITY\_MUC  
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : N.GeneSeq\_101002:\*

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2: /SIDS2/gcgdata/geneSeq/geneSeqn-emb1/NA1981.DAT:\*  
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22: /SIDS2/gcgdata/geneSeq/geneSeqn-emb1/NA2001A.DAT:\*  
23: /SIDS2/gcgdata/geneSeq/geneSeqn-emb1/NA2001B.DAT:\*  
24: /SIDS2/gcgdata/geneSeq/geneSeqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description                 |
|------------|-------|-------------|--------|----|-----------------------------|
| 1          | 600   | 100.0       | 600    | 21 | AAA96856 Nucleotide sequenc |
| 2          | 373.6 | 62.3        | 462    | 21 | AAA96854 Nucleotide sequenc |
| 3          | 312.2 | 52.0        | 604    | 21 | AAA96857 Nucleotide sequenc |
| 4          | 304.6 | 50.8        | 393    | 21 | AAA96853 Nucleotide sequenc |
| 5          | 281.4 | 46.9        | 541    | 21 | AAA96858 Nucleotide sequenc |
| 6          | 234.2 | 39.0        | 392    | 21 | AAA96855 Nucleotide sequenc |
| 7          | 212.4 | 35.4        | 317    | 21 | AAA96837 Nucleotide sequenc |
| 8          | 212.4 | 35.4        | 472    | 21 | AAA96859 Nucleotide sequenc |
| 9          | 200.4 | 33.4        | 348    | 21 | AAA96838 Nucleotide sequenc |

|    |       |      |       |    |                               |
|----|-------|------|-------|----|-------------------------------|
| 10 | 152.8 | 25.5 | 371   | 21 | AAA96839 Nucleotide sequenc   |
| 11 | 140.8 | 23.5 | 301   | 21 | AAA96841 Nucleotide sequenc   |
| 12 | 140.8 | 23.5 | 398   | 21 | AAA96840 Nucleotide sequenc   |
| 13 | 120.6 | 20.1 | 392   | 19 | AAV14019 CsVMV promoter CVP   |
| 14 | 120.6 | 20.1 | 411   | 19 | AAV14021 CsVMV promoter PB.   |
| 15 | 120.6 | 20.1 | 515   | 21 | AAA96836 Promoter from Inte   |
| 16 | 120.6 | 20.1 | 515   | 22 | AAFS5505 Nucleotide sequenc   |
| 17 | 120.6 | 20.1 | 524   | 19 | AAV14020 CsVMV promoter CVP   |
| 18 | 120.6 | 20.1 | 526   | 19 | AAV14018 CsVMV promoter PA.   |
| 19 | 120.6 | 20.1 | 532   | 22 | AAAD11575 Cassava Vein Mosaic |
| 20 | 120.6 | 20.1 | 853   | 22 | AAFS5506 Nucleotide sequenc   |
| 21 | 120.6 | 20.1 | 1839  | 24 | ABL57988 4-Hydroxyphenylpyr   |
| 22 | 120.6 | 20.1 | 4677  | 24 | ABL57989 4-Hydroxyphenylpyr   |
| 23 | 120.6 | 20.1 | 8187  | 24 | ABL58082 4-Hydroxyphenylpyr   |
| 24 | 120.6 | 20.1 | 8340  | 24 | ABA04755 Binary vector pAG1   |
| 25 | 120.6 | 20.1 | 8340  | 24 | AAAD24139 pAD14002 Binary ve  |
| 26 | 120.6 | 20.1 | 12241 | 24 | ABO73049 Tomato anthocyanin   |
| 27 | 120.6 | 20.1 | 12241 | 24 | AAAD36732 Binary vector DNA   |
| 28 | 117.4 | 19.6 | 305   | 19 | AAV14022 CsVMV promoter PC.   |
| 29 | 117.4 | 19.6 | 420   | 19 | AAV14026 CsVMV promoter pde   |
| 30 | 117.4 | 19.5 | 476   | 19 | AAV14053 CsVMV promoter. C    |
| 31 | 115.8 | 19.3 | 593   | 22 | AAFS5507 Nucleotide sequenc   |
| 32 | 115.8 | 19.3 | 857   | 22 | AAFS5508 Nucleotide sequenc   |
| 33 | 115.8 | 19.3 | 931   | 22 | AAFS5509 Nucleotide sequenc   |
| 34 | 115.4 | 19.2 | 931   | 22 | AAFS5510 Nucleotide sequenc   |
| 35 | 115.4 | 19.2 | 931   | 22 | AAFS5510 Nucleotide sequenc   |
| 36 | 81.8  | 13.6 | 482   | 19 | AAV14027 CsVMV promoter pde   |
| 37 | 81.8  | 13.5 | 441   | 19 | AAV14033 CsVMV promoter pde   |
| 38 | 80    | 13.3 | 243   | 21 | AAA96835 Promoter from Inte   |
| 39 | 79.6  | 13.3 | 491   | 19 | AAV14030 CsVMV promoter pde   |
| 40 | 75.4  | 12.6 | 392   | 21 | AAA96855 Nucleotide sequenc   |
| 41 | 74    | 12.3 | 261   | 19 | AAV14023 CsVMV promoter pde   |
| 42 | 69.6  | 11.6 | 79    | 21 | AAA96848 Nucleotide desoxy    |
| 43 | 69.6  | 11.6 | 79    | 21 | AAA96472 Nucleotide sequenc   |
| 44 | 69.6  | 11.6 | 296   | 21 | AAA96465 Nucleotide sequenc   |
| 45 | 69    | 11.5 | 259   | 21 | AAA96477 Nucleotide sequenc   |

## ALIGNMENTS

RESULT 1

AAA96856

19-FEB-2001 (first entry)

AAA96856 strand; DNA: 600 BP.

AAA96856;

19-FEB-2001 (first entry)

Nucleotide sequence of chimeric expression promoter MPr1165.

Promoter: intergenic region; Commelina yellow mottle virus;

chimeric expression promoter; plant vascular expression promoter;

plant green tissue expression promoter; Cassava vein mosaic virus;

transgenic plant; chimera; ss.

Chimeric - Commelina yellow mottle virus.

Chimeric - Cassava vein mosaic virus.

WO200058485-A1.

05-OCT-2000.

29-MAR-2000; 2000WO-IB00370.

29-MAR-1999; 99FR-0003925.

(MER1-) MERISTEM THERAPEUTICS.

Rance I, Gruber V, Theisen M;

WPI; 2000-647238/62.

PT Chimeric expression promoter for transgenic plant production, comprises  
 PT sequence from promoter comprising vascular expression region replaced  
 PT with sequence from promoter comprising green tissue expression region  
 PT -  
 PX  
 PX Claim 5; Page 86-87; 91pp; English.  
 PS  
 XX  
 XX The present sequence represents a chimeric promoter of the invention.  
 CC The specification describes chimeric expression promoters. These  
 CC chimeric promoters comprise a nucleic acid sequence which is derived  
 CC from a first plant promoter, in which a plant vascular expression  
 CC promoter region is replaced with a nucleic acid sequence derived from  
 CC a second plant promoter comprising a plant green tissue expression  
 CC promoter region. Preferably, the first plant promoter originates from  
 CC Comellina yellow mottle virus, and the second plant promoter originates  
 CC from the Casava vein mosaic virus. Especially, the promoters are  
 CC derived from transgenic plants. The chimeric promoters are useful  
 CC for producing transgenic plants.  
 CC  
 XX Sequence 600 BP; 188 A; 111 C; 147 G; 154 T; 0 other;  
 50

|                           |         |                     |           |             |
|---------------------------|---------|---------------------|-----------|-------------|
| Query Match               | 100.0%  | Score 600;          | DB 21;    | Length 600; |
| Best Local Similarity     | 100.0%; | Pred. No. 9.2e-174; |           |             |
| Matches 600; Conservative | 0;      | Mismatches 0;       | Indels 0; | Gaps 0;     |

|    |     |  |     |
|----|-----|--|-----|
| Oy | 1   | AACTTGATGCGCGAGCGACCTAGTAATCCGCCGTCATGCATATGACATCATACAGTACTGA    | 60  |
| Dp | 1   | AAGCTTGATCCCTCGACGACCTAGTAATCCGCCGTCATGCATATGACATCATACAGTACTGA   | 60  |
| Oy | 61  | GGAGATGAAATAGCTAAGCCATGACACTCTGTGTGCGAATATTGAAGACGTAAGCACTGACGAC | 120 |
| Dp | 61  | GGAGATGAAATAGCTAAGCCATGACACTCTGTGTGCGAATATTGAAGACGTAAGCACTGACGAC | 120 |
| Oy | 121 | AACAATGAAAGAGAAAGATTAAGTGAAGAGACATTAAGAGACATATGA                 | 180 |
| Dp | 121 | AACAATGAAAGAGAAAGATTAAGTGAAGAGACATTAAGAGACATATGA                 | 180 |
| Oy | 181 | AGGTGGAATATGTAAGGGCGGAAAGTAACTTAAGCATTTTGTAATTTGGTTAGACTAGT      | 240 |
| Dp | 181 | AGGTGGAATATGTAAGGGCGGAAAGTAACTTAAGCATTTTGTAATTTGGTTAGACTAGT      | 240 |
| Oy | 241 | GATTGATGTGATATCAAGATTAAGTATATCTCCACTGACGTAAAGGATGACGCAATGCC      | 300 |
| Dp | 241 | GATTGATGTGATATCAAGATTAAGTATATCTCCACTGACGTAAAGGATGACGCAATGCC      | 300 |
| Oy | 301 | ACGACTAGTGAATGTGATATCAAGATTAAGTATATCTCCACTGACGTAAAGGATG          | 360 |
| Dp | 301 | ACGACTAGTGAATGTGATATCAAGATTAAGTATATCTCCACTGACGTAAAGGATG          | 360 |
| Oy | 361 | ACGCATGCCACGACTAGTGAATGTGATATCAAGTATATGATGTATATCCACTGACG         | 420 |
| Dp | 361 | ACGCATGCCACGACTAGTGAATGTGATATCAAGTATATGATGTATATCCACTGACG         | 420 |
| Oy | 421 | TAAAGGATGAGCATATGCCACACATAGATTAAGTATCAAGATTAAGTATGATATCT         | 480 |
| Dp | 421 | TAAAGGATGAGCATATGCCACACATAGTATTAAGTATCAAGATTAAGTATGATATCT        | 480 |
| Oy | 481 | CCACTGACGTAAAGGATGACGCATGCCACGTTACCCGGTATGCCGGTTTCCCAAGCTTAT     | 540 |
| Dp | 481 | CCACTGACGTAAAGGATGACGCATGCCACGTTACCCGGTATGCCGGTTTCCCAAGCTTAT     | 540 |
| Oy | 541 | TTCTCTATTTAAGCACTTTGTGTAGTACGTTAAGAAACCAACACACACACTAGAGATCC      | 600 |
| Dp | 541 | TTCTCTATTTAAGCACTTTGTGTAGTACGTTAAGAAACCAACACACACACTAGAGATCC      | 600 |

|          |                                 |
|----------|---------------------------------|
| RESULT 2 |                                 |
| AAA96854 |                                 |
| ID       | AAA96854 standard; DNA; 462 BP. |
| XX       |                                 |
| AC       |                                 |
| XX       | AAA96854;                       |
| DT       | 19-FEB-2001 (first entry)       |

XX Nucleotide sequence of chimeric expression promoter MP1163.  
DE  
XX  
XX Promoter; intergenic region; Commelina yellow mottle virus;  
KW chimeric expression promoter; plant vascular expression promoter;  
KW plant green tissue expression promoter; Cassava vein mosaic virus;  
KW transgenic plant; chimera, ss.  
XX  
OS Chimeric - Commelina yellow mottle virus.  
OS Chimeric - Cassava vein mosaic virus.  
PN  
XX  
XX WO200058485-A1.  
PD  
XX 05-OCT-2000.  
XX  
XX 29-MAR-2000; 2000WO-IB00370.  
PF  
XX  
XX 29-MAR-1999; 99FR-0003925.  
PR  
XX  
XX (MERI-) MERISTEM THERAPEUTICS.  
PA  
XX  
XX Rance I, Gruber V, Theisen M,  
PI  
XX  
XX MPI; 2000-647238/62.  
DR

PT Chimeric expression promoter for transgenic plant production, comprises  
PT sequence from promoter comprising vascular expression region replaced  
PT with sequence from promoter comprising green tissue expression region  
XX -  
PS Claim 5, page 86, 91pp; English.

The present sequence represents a chimeric promoter of the invention. The specification describes chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from *Combellina* yellow mottle virus, and the second plant promoter originates from the cassava vein mosaic virus. Especially, the promoters are derived from intergenic regions. The chimeric promoters are useful for producing transgenic plants.

Sequence 462 BP; 148 A; 87 C; 111 G; 116 T; 0 other;

|                           |        |                   |           |             |
|---------------------------|--------|-------------------|-----------|-------------|
| Query Match               | 62.38; | Score 373.6;      | DB 21;    | Length 462; |
| Best Local Similarity     | 95.38; | Pred. No. 2e-104; |           |             |
| Matches 385; Conservative | 0;     | Mismatches 19;    | Indels 0; | Gaps 0;     |

|    |     |  |     |
|----|-----|--|-----|
| Qy | 1   | AAGCTTCATGCGCTGCGACAGCTAGTATCCGCCGTCATCAATGACATCATCAGACTACTGA  | 60  |
|    |     |  |     |
|    |     |  |     |
|    |     |  |     |
| Db | 1   | AAGCTTGCATGCGCTGCACAGCTAGTATCCGCCGTCATCAATGACATCATCAGACTACTGA  | 60  |
|    |     |  |     |
|    |     |  |     |
|    |     |  |     |
| Qy | 61  | GGAGTGAATAGCTAGCCATGACACTCTGTGTCCGAATATATGAAGACGTAAAGCACTGAGAC | 120 |
|    |     |  |     |
|    |     |  |     |
|    |     |  |     |
| Db | 61  | GGAGTGAATAGCTAGCCATGACACTCTGTGTCCGAATATATGAAGACGTAAAGCACTGAGAC | 120 |
|    |     |  |     |
|    |     |  |     |
|    |     |  |     |
| Qy | 121 | AACATATGAAGAAGACAATATAAAGTCGGTGTATTTGGAAGAGCAATATAGAGACACATGTA | 180 |
|    |     |  |     |
|    |     |  |     |
|    |     |  |     |
| Db | 121 | AACATATGAAGAAGACAATATAAAGTCGGTGTATTTGGAAGAGCAATATAGAGACACATGTA | 180 |
|    |     |  |     |
|    |     |  |     |
|    |     |  |     |
| Qy | 181 | AGGTGAAATCTAAGGCGCGAAGTAACCTTATGCAATTTTGAATTTGGTTACACTAGT      | 240 |
|    |     |  |     |
|    |     |  |     |
|    |     |  |     |
| Db | 181 | AGGTGAAATCTAAGGCGCGAAGTAACCTTATGCAATTTTGAATTTGGTTACACTAGT      | 240 |
|    |     |  |     |
|    |     |  |     |
|    |     |  |     |
| Qy | 241 | GATTGATGTGATATCAGATTGATGTGATATCTCCACTGACGTAAAGGATAGCAGATGCC    | 300 |
|    |     |  |     |
|    |     |  |     |
|    |     |  |     |
| Db | 241 | GATTGATGTGATATCAGATTGATGTGATATCTCCACTGACGTAAAGGATAGCAGATGCC    | 300 |
|    |     |  |     |
|    |     |  |     |
|    |     |  |     |
| Qy | 301 | ACGACTAGTGAATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATG      | 360 |
|    |     |  |     |
|    |     |  |     |
|    |     |  |     |
| Db | 301 | ACGACTAGTGAATGTGATATCAAGATTGATGTGATATCTCCACTGACGTAAAGGATG      | 360 |
|    |     |  |     |
|    |     |  |     |
|    |     |  |     |

Oy 361 AGCATGCCAGACTAGTATGATATCAAGATTGATG 404  
 |||||  
 Db 361 AGCATGCCAGCTTACCGGATGCGGTTCCCAAGCTTTATTT 404

## RESULT 3

AAA96857  
 ID AAA96857 standard; DNA; 604 BP.

XX AAA96857;  
 AC  
 XX  
 DT

19-FEB-2001 (first entry)

DE Nucleotide sequence of chimeric expression promoter MP1167.

XX  
 KW Promoter; intergenic region; Commelina yellow mottle virus;  
 KW chimeric expression promoter; plant vascular expression promoter;  
 KW plant green tissue expression promoter; Cassava vein mosaic virus;  
 KW transgenic plant; chimera; ss.

XX Chimeric - Commelina yellow mottle virus.

OS Chimeric - Cassava vein mosaic virus.

XX WO200058485-A1.

XX 05-OCT-2000.

XX 29-MAR-2000; 2000WO-IB00370.

XX 29-MAR-1999; 99FR-0003925.

XX (MERI-) MERISTEM THERAPEUTICS.

XX Rance I, Gruber V, Theisen M;

DR WPI; 2000-647238/62.

XX Chimeric expression promoter for transgenic plant production, comprises  
 PT sequence from promoter comprising vascular expression region replaced  
 PT with sequence from promoter comprising green tissue expression region

PS Claim 5; Page 87; 91pp; English.

XX The present sequence represents a chimeric promoter of the invention.  
 CC The specification describes chimeric expression promoters. These  
 CC chimeric promoters comprise a nucleic acid sequence which is derived  
 CC from a first plant promoter, in which a plant vascular expression  
 CC promoter region is replaced with a nucleic acid sequence derived from  
 CC a second plant promoter comprising a plant green tissue expression  
 CC promoter region. Preferably, the first plant promoter originates from  
 CC Commelina yellow mottle virus, and the second plant promoter originates  
 CC from the Cassava vein mosaic virus. Especially, the promoters are  
 CC derived from intergenic regions. The chimeric promoters are useful  
 CC for producing transgenic plants.

XX Sequence 604 BP; 186 A; 116 C; 145 G; 157 T; 0 other;

Query Match 52.0%; Score 312.2; DB 21; Length 604;  
 Best Local Similarity 84.5%; Pred. No. 1.4e-85;  
 Matches 442; Conservative 0; Mismatches 3; Indels 78; Gaps 5;

Oy 78 CATGACACTGTGCGAATATTGAAGACGTAGACGACGACCAATGAAGAGAA 137  
 |||||  
 Db 160 CATGCACTGTGCGAATATTGAAGACGTAGACGACGACCAATGAAGAGAA 219

Oy 138 GATAGGCGGTGATTTGAAGAGACATAGAGACATGTAAAGTGAAGAAATAGG 197  
 |||||

Db 220 GATTAAGTGGGATTTG-AGAGACATAGAGACATGTAAAGTGAAGAAATAGG 278

Oy 198 GCGAAGATTAACCTTATCATTTGTAATTTGGTTACGACTAGTGTATGATATCA 257  
 |||||

Db 279 GCGAAGATTAACCTTATCATTTGTAATTTGGTTAC----- 314

Oy 258 GATTATGATGATATCTCCACGTAGCSTAAAGGATGACGATGCCAGACTAGTATG 317  
 |||||

Db 315 -----CTAGTATGATG 327

Oy 318 TGATATCAAGATTGATGATATCTCCACGTAGCSTAAAGGATGACGATG 377  
 |||||

Db 328 TGATATCAAGATTGATGATATCTCCACGTAGCSTAAAGGATGACGATG 385  
 |||||

Oy 378 TGATGATGTGATATCAAGATTGATGATATCTCCACGTAGCSTAAAGGATGACGATG 437  
 |||||

Db 386 TGATGATGTGATATCAAGATTGATGATATCTCCACGTAGCSTAAAGGATGACGATG 445  
 |||||

Oy 438 CACGACTAGTATGATGATATCAAGATTGATGATATCTCCACGTAGCSTAAAGGAT 497  
 |||||

Db 446 CAC--CTAGTATGATGATGATATCAAGATTGATGATATCTCCACGTAGCSTAAAGGAT 503  
 |||||

Oy 498 GACGATGCCAGCTTACCGGATGCGGTTCCCAAGCTTTATTTCTTATTAAGCACT 557  
 |||||

Db 504 GACGATGCCAGCTTACCGGATGCGGTTCCCAAGCTTTATTTCTTATTTAA--ACT 561  
 |||||

Oy 558 TGTGTAGTAGCTTAGAAAAACCAACCAACCTAGAGATCC 600

Db 562 TGTGTAGTAGCTTAGAAAAACCAACCAACCTAGAGATCC 604

## RESULT 4

AAA96853  
 ID AAA96853 standard; DNA; 393 BP.

XX AAA96853;  
 AC  
 XX  
 DT

19-FEB-2001 (first entry)

DE Nucleotide sequence of chimeric expression promoter MP1162.

KW Promoter; intergenic region; Commelina yellow mottle virus;

KW chimeric expression promoter; plant vascular expression promoter;

KW plant green tissue expression promoter; Cassava vein mosaic virus;

XX transgenic plant; chimera; ss.

OS Chimeric - Commelina yellow mottle virus.

XX Chimeric - Cassava vein mosaic virus.

XX WO200058485-A1.

XX 05-OCT-2000.

XX 29-MAR-2000; 2000WO-IB00370.

XX 29-MAR-1999; 99FR-0003925.

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DR WPI; 2000-647238/62.

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 PT with sequence from promoter comprising green tissue expression region

PS Claim 5; Page 85; 91pp; English.

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 CC chimeric promoters comprise a nucleic acid sequence which is derived  
 CC from a first plant promoter, in which a plant vascular expression  
 CC promoter region is replaced with a nucleic acid sequence derived from  
 CC a second plant promoter comprising a plant green tissue expression  
 CC promoter region. Preferably, the first plant promoter originates from

CC Commelina yellow mottle virus, and the second plant promoter originates  
CC from the cassava vein mosaic virus. Especially, the promoters are  
CC derived from intergenic regions. The chimeric promoters are useful  
CC for producing transgenic plants.

SO Sequence 393 BP; 128 A; 75 C; 93 G; 97 T; 0 other;

Query Match 50.8%; Score 304.6; DB 21; Length 393;  
Best Local Similarity 94.3%; Pred. No. 2.6e-83;  
Matches 316; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 AACCTGCAATGCTGACGACCTGATCCCGTCATCAATGACATCATCAGTACTGA 60  
DB 1 AACCTGCAATGCTGACGACCTGATCCCGTCATCAATGACATCATCAGTACTGA 60  
QY 61 GGAGATGAATAGTACGACGACCTGTCGCAATTTGAAGCCGTAACGACGAC 120  
DB 61 GGAGATGAATAGTACGACGACCTGTCGCAATTTGAAGCCGTAACGACGAC 120  
QY 121 AACATGMAAAGAAAGATAGTGGTGTGTAAGAGACATAGAGACATGTA 180  
DB 121 AACATGMAAAGAAAGATAGTGGTGTGTAAGAGACATAGAGACATGTA 180  
QY 181 AGGTGMAAATGTAAGGCGGAAAGTAACTTATGCAATTTGTTAGACTAGT 240  
DB 181 AGGTGMAAATGTAAGGCGGAAAGTAACTTATGCAATTTGTTAGACTAGT 240  
QY 241 GATTGATGATATCAAGATTTGATATCCCACTGACGTAAGGATGACGACATGCC 300  
DB 241 GATTGATGATATCAAGATTTGATATCCCACTGACGTAAGGATGACGACATGCC 300  
QY 301 ACGACTAGTATGATGTGATATCAAGATTTGATGT 335  
DB 301 ACGTAAACCGGTATGCCGGTTCCCAAGCTTTATTT 335

RESULT 5  
AAA96858 standard; DNA; 541 BP.

AC AAA96858;

DT 19-FEB-2001 (first entry)

DE Nucleotide sequence of chimeric expression promoter Mp1168.

KW Promoter; intergenic region; Commelina yellow mottle virus;

KW chimeric expression promoter; plant vascular expression promoter;  
KW plant green tissue expression promoter; Cassava vein mosaic virus;  
KW transgenic plant; chimera; ss.

OS Chimeric - Commelina yellow mottle virus.  
OS Chimeric - Cassava vein mosaic virus.

PN WO200058485-A1.

PD 05-OCT-2000.

PF 29-MAR-2000; 2000WO-IB00370.

PR 29-MAR-1999; 99FR-0003925.

PA (MERI-) MERISTEM THERAPEUTICS.

PI Rance I, Gruber V, Theisen M;

DR WPI: 2000-647238/62.

XX Chimeric expression promoter for transgenic plant production, comprises  
PT sequence from promoter comprising vascular expression region, replaced  
PT with sequence from promoter comprising green tissue expression region  
XX

PS Claim 5; Page 87-88; 91pp; English.

XX The present sequence represents a chimeric promoter of the invention.  
CC The specification describes chimeric expression promoters. These  
CC The specification describes chimeric expression promoters. These  
CC chimeric promoters comprise a nucleic acid sequence which is derived  
CC from a first plant promoter, in which a plant vascular expression  
CC promoter region is replaced with a nucleic acid sequence derived from  
CC a second plant promoter comprising a plant green tissue expression  
CC promoter region. Preferably, the first plant promoter originates from  
CC Commelina yellow mottle virus, and the second plant promoter originates  
CC from the cassava vein mosaic virus. Especially, the promoters are  
CC derived from intergenic regions. The chimeric promoters are useful  
CC for producing transgenic plants.

SO Sequence 541 BP; 169 A; 104 C; 130 G; 138 T; 0 other;

Query Match 46.9%; Score 281.4; DB 21; Length 541;  
Best Local Similarity 93.3%; Pred. No. 3.8e-76;  
Matches 305; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 78 CATGACACTGTCGCAATTTGAAGACGTAACGACGACACATGMAAAGAA 137  
DB 160 CATGCACTCTGCGCAATTTGAAGACGTAACGACGACACATGMAAAGAA 219  
QY 138 GATAGGTCGCTGATTTGTGAAGACATAGAGACATGTAAGGTGMAAATGTAAG 197  
DB 220 GATAGGTCGCTGATTTGTG- AAGAGACATAGAGACATGTAAGGTGMAAATGTAAG 278  
QY 198 GCGGAAAGTAACTTATGCAATTTGTTAGACTAGTATGATATCA 257  
DB 279 GCGGAAAGTAACTTATGCAATTTGTTAGACTAGTATGATATCA 338  
QY 258 GATTGATGATATCAAGATTTGATATCCCACTGACGTAAGGATGACGACATGATTTGATG 317  
DB 339 GATTGATGATATCAAGATTTGATATCCCACTGACGTAAGGATGACGACATGATTTGATG 398  
QY 318 TGATATCAAGATTTGATATCTCCACTGACGTAAGGATGACGACATG 377  
DB 399 TGATATCAAGATTTGATATCTCCACTGACGTAAGGATGACGACATG 458  
QY 378 TGATATGATGATATCAAGATTTGATGT 404  
DB 459 CGGTATGCTGTTCCCAAGCTTTATTT 485

RESULT 6  
AAA96855 standard; DNA; 392 BP.

AC AAA96855;

DT 19-FEB-2001 (first entry)

DE Nucleotide sequence of chimeric expression promoter Mp1164.

KW Promoter; intergenic region; Commelina yellow mottle virus;

KW chimeric expression promoter; plant vascular expression promoter;  
KW plant green tissue expression promoter; Cassava vein mosaic virus;  
KW transgenic plant; chimera; ss.

OS Chimeric - Commelina yellow mottle virus.  
OS Chimeric - Cassava vein mosaic virus.

PN WO200058485-A1.

PD 05-OCT-2000.

PF 29-MAR-2000; 2000WO-IB00370.

PR 29-MAR-1999; 99FR-0003925.

PA (MERI-) MERISTEM THERAPEUTICS.

XX



|    |   |  |    |
|----|---|--|----|
| XX | 29-MAR-1999:  | 99FR-0003925.                          |    |
| PR |   |  |    |
| XX | (MERI-) MERISTEM THERAPEUTICS.  |  |    |
| PA |   |  |    |
| XX | Rance I, Gruber V, Thelsen M;   |  |    |
| PI |   |  |    |
| XX | WPI: 2000-647238/62.  |  |    |
| DR |   |  |    |
| XX |   |  |    |
| PT | Chimeric expression promoter for transgenic plant production, comprises |  |    |
| PT | sequence from promoter comprising vascular expression region replaced   |  |    |
| PT | with sequence from promoter comprising green tissue expression region   |  |    |
| XX |   |  |    |
| PS | Claim 5; Page 81; 91pp; English.  |  |    |
| XX |   |  |    |
| CC | The present sequence represents a chimeric promoter of the invention.   |  |    |
| CC | The specification describes chimeric expression promoters. These        |  |    |
| CC | chimeric promoters comprise a nucleic acid sequence which is derived    |  |    |
| CC | from a first plant promoter, in which a plant vascular expression       |  |    |
| CC | promoter region is replaced with a nucleic acid sequence derived from   |  |    |
| CC | a second plant promoter comprising a plant green tissue expression      |  |    |
| CC | promoter region. Preferably, the first plant promoter originates from   |  |    |
| CC | Commelina yellow mottle virus, and the second plant promoter originates |  |    |
| CC | from the Cassava vein mosaic virus. Especially, the promoters are       |  |    |
| CC | derived from intergenic regions. The chimeric promoters are useful      |  |    |
| CC | for producing transgenic plants.  |  |    |
| XX |   |  |    |
| XX | Sequence 317 BP: 107 A; 61 C; 74 G; 75 T; 0 other:                      |  |    |
| XX |   |  |    |
| XX | Query Match   | 35.4%; Score 212.4; DB 21; Length 317; |    |
| XX | Best Local Similarity   | 99.5%; Pred. No. 4.2e-55;              |    |
| XX | Matches 213; Conservative   | 0; Mismatches 1; Indels 0; Gaps        | 0; |
| XX |   |  |    |
| QY | 20 ACTGATCGCCCGCTCATCATGACATCATCAGTACTGAGGAGATAATAGCTAGCCA              | 79                                     |    |
| DB | 18 ACTGATCGCCCGCTCATCATGACATCATCAGTACTGAGGAGATAATAGCTAGCCA              | 77                                     |    |
| QY | 80 TGACACCTCTGGCAATATTGAAGCGTAAACGTAACGACGACAAATGAAAGAAAGA              | 139                                    |    |
| DB | 78 TGACACCTCTGGCAATATTGAAGCGTAAACGTAACGACGACGACAAATGAAAGAAAGA           | 137                                    |    |
| QY | 140 TAAAGTCGTGATTTGTGAAGACATAGAGACATGTAAGTGAATAATGTAAGGC                | 199                                    |    |
| DB | 138 TAAAGTCGTGATTTGTGAAGACATAGAGACATGTAAGTGAATAATGTAAGGC                | 197                                    |    |
| QY | 200 GGAAGTAACCTTATGCATTGTGTAATTTGGTTAC                                  | 233                                    |    |
| DB | 198 GGAAGTAACCTTATGCATTGTGTAATTTGGTTAC                                  | 231                                    |    |
| XX |   |  |    |
| XX | RESULT 8  |  |    |
| XX | AAA96859  |  |    |
| XX | AAA96859 standard; DNA: 472 BP.   |  |    |
| XX | AAA96859;   |  |    |
| XX |   |  |    |
| DT | 19-FEB-2001 (first entry)   |  |    |
| DE | Nucleotide sequence of chimeric expression promoter MP1169.             |  |    |
| XX |   |  |    |
| KM | Promoter; intergenic region; Commelina yellow mottle virus;             |  |    |
| KM | chimeric expression promoter; plant vascular expression promoter;       |  |    |
| KM | plant green tissue expression promoter; Cassava vein mosaic virus;      |  |    |
| XX | transgenic plant; chimera; ss.  |  |    |
| XX |   |  |    |
| OS | Chimeric - Commelina yellow mottle virus.                               |  |    |
| OS | Chimeric - Cassava vein mosaic virus.                                   |  |    |
| XX |   |  |    |
| PN | WO200058485-A1.   |  |    |
| XX |   |  |    |
| XX | 05-OCT-2000.  |  |    |

|                       |        |              |          |            |     |        |      |
|-----------------------|--------|--------------|----------|------------|-----|--------|------|
| Query Match           | 35.48; | Score        | 212.4;   | DB         | 21; | Length | 472; |
| Best Local Similarity | 91.58; | Pred. No.    | 4.9e-55; |            |     |        |      |
| Matches               | 236;   | Conservative | 0;       | Mismatches | 21; | Indels | 1;   |
|                       |        |              |          |            |     | Gaps   | 1;   |

RESULT 9  
AAA96838  
ID AAA96838 standard; DNA; 348 BP.

DE Nucleotide sequence of chimeric expression promoter MPr1117.

|    |   |
|----|---|
| KM | Promoter, intergenic region; Commelina yellow mottle virus;       |
| KM | Chimeric expression promoter; plant vascular expression promoter; |
| KM | plant green tissue expression promoter; Cassava vein mosaic virus |
| KM | transgenic plant; chimera; ss.                                    |
| XX |   |
| OS | Chimeric - Commelina yellow mottle virus.                         |
| OS | Chimeric - Cassava vein mosaic virus.                             |

PS Claim 5; Page 81; 91pp; English

**SQ** Sequence 348 BP; 116 A; 70 C; 78 G; 84 T; 0 other.

|                       |       |  |             |            |    |        |     |      |
|-----------------------|-------|--|-------------|------------|----|--------|-----|------|
| Query Match           | 33.4% | Score  | 200.4       | DB         | 21 | Length | 348 |      |
| Best Local Similarity | 99.1% | Pred   | NO. 2.1e-51 |            |    |        |     |      |
| Matches               | 212   | Conservative   | 0           | Mismatches | 1  | Indels | 1   | Gaps |
| QY                    | 20    | ACTAGTATCCGGCGCTGCATCAATGACATCATCATGACTACTGAGAGATGTAATGATGCCA  | 79          |            |    |        |     |      |
|                       | 52    | ACTAGTATCCGGCGCTGCATCAATGACATCATCATGACTACTGAGAGATGTAATGATGCCA  | 111         |            |    |        |     |      |
| QY                    | 80    | TGACACTCTGTGCCAATATTGAAAGCGTAAAGCATTGACAGACAACAATGAAAAAGAGAA   | 139         |            |    |        |     |      |
|                       | 112   | TGACACTCTGTGCCAATATTGAAAGCGTAAAGCATTGACAGACAACAATGAAAAAGAGAA   | 171         |            |    |        |     |      |
| QY                    | 140   | TAAAGTCGGGTATTGTGAAGAGACATAGAGACACATTAAGGTTGGAATAATGTAAGGGC    | 199         |            |    |        |     |      |
|                       | 172   | TAAAGTCGGGTATTGTG-TAAGAGACATGAGAGACACATTAAGGTTGGAATAATGTAAGGGC | 230         |            |    |        |     |      |
| QY                    | 200   | GGAAGTAACTTATGCATTTGTAATTTGGCTTAC                              | 233         |            |    |        |     |      |
|                       | 231   | GGAAGTAACTTATGCATTTGTAATTTGGCTTAC                              | 264         |            |    |        |     |      |

|           |                                |
|-----------|--------------------------------|
| RESULT 10 |                                |
| AAA96839  |                                |
| ID        | AAA96839 standard; DNA; 371 BP |

DE Nucleotide sequence of chimeric expression promoter MPr1146.

KM Promoter; intergenic region; *Commelina* yellow mottle virus;  
KM chlorotic expression promoter; plant vascular expression promoter;  
KM plant green tissue expression promoter; Cassava vein mosaic virus  
transgenic plant; chimera; ss

OS chimeric - Commelina yellow mottle virus

```
OS Chimeric - Cassava vein mosaic virus.
XX
XX WO200058485-A1.
XX
XX 05-OCT-2000.
XX
XX 29-MAR-2000; 2000WO-IB00370.
XX
XX 29-MAR-1999; 99FR-0003925.
XX
XX (MERI-) MERISTEM THERAPEUTICS.
XX
XX Rance I, Gruber V, Theisen M;
XX
XX WPI: 2000-647238/62.
XX
XX Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
XX
XX Claim 5; Page 81; 91pp; English.
XX
XX The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
XX Sequence 371 BP; 122 A; 68 C; 89 G; 92 T; 0 other;
SQ
Query Match 25.5%; Score 152.8; DB 21; Length 371;
Best Local Similarity 98.7%; Pred. No. 8.2e-37;
Matches 154; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 78 CATGACACTCTGTGCGAATATTGAAGACGTAGCAGCACAACATGAAAGAGAA 137
DB 130 CATGCACTCTGTGCGAATATTGAAGACGTAGCAGCACAACATGAAAGAGAA 189
OY 138 GATTAAGTCGGTGAATTTGAAAGACATAGAGACACATGTAAAGTGAATGTAAAG 197
DB 190 GATTAAGTCGGTGAATTTGAAAGACATAGAGACACATGTAAAGTGAATGTAAAG 249
OY 198 GCGGAAAGTAACCTTATGCATTGTGAATTTGGTTAC 233
DB 250 GCGGAAAGTAACCTTATGCATTGTGAATTTGGTTAC 285
RESULT 11
ID AAA96841
ID AAA96841 standard; DNA; 301 BP.
XX
XX AAA96841;
XX
XX 19-FEB-2001 (first entry)
XX
XX Nucleotide sequence of chimeric expression promoter MPr1154.
XX
XX Promoter: intergenic region; Commelina yellow mottle virus;
KW chimeric expression promoter; plant vascular expression promoter;
KW plant green tissue expression promoter; Cassava vein mosaic virus;
KW transgenic plant; chimera; ss.
XX
XX Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
XX WO200058485-A1.
XX
XX
```

```
XX
XX 05-OCT-2000.
XX
XX 29-MAR-2000; 2000WO-IB00370.
XX
XX 29-MAR-1999; 99FR-0003925.
XX
XX (MERI-) MERISTEM THERAPEUTICS.
XX
XX Rance I, Gruber V, Theisen M;
XX
XX WPI: 2000-647238/62.
XX
XX Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
XX
XX Claim 5; Page 82; 91pp; English.
XX
XX The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
XX Sequence 301 BP; 98 A; 54 C; 74 G; 75 T; 0 other;
SQ
Query Match 23.5%; Score 140.8; DB 21; Length 301;
Best Local Similarity 98.1%; Pred. No. 3.6e-33;
Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
OY 78 CATGACACTCTGTGCGAATATTGAAGACGTAGCAGCACAACATGAAAGAGAA 137
DB 63 CATGCACTCTGTGCGAATATTGAAGACGTAGCAGCACAACATGAAAGAGAA 122
OY 138 GATTAAGTCGGTGAATTTGAAAGACATAGAGACACATGTAAAGTGAATGTAAAG 197
DB 123 GATTAAGTCGGTGAATTTG - AAGAGACATAGAGACACATGTAAAGTGAATGTAAAG 181
OY 198 GCGGAAAGTAACCTTATGCATTGTGAATTTGGTTAC 233
DB 182 GCGGAAAGTAACCTTATGCATTGTGAATTTGGTTAC 217
RESULT 12
ID AAA96840
ID AAA96840 standard; DNA; 398 BP.
XX
XX AAA96840;
XX
XX 19-FEB-2001 (first entry)
XX
XX Nucleotide sequence of chimeric expression promoter MPr1147.
XX
XX Promoter: intergenic region; Commelina yellow mottle virus;
KW chimeric expression promoter; plant vascular expression promoter;
KW plant green tissue expression promoter; Cassava vein mosaic virus;
KW transgenic plant; chimera; ss.
XX
XX Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
XX WO200058485-A1.
XX
XX 05-OCT-2000.
XX
XX
```

PF 29-MAR-2000; 2000MO-IB00370.  
XX  
PR 29-MAR-1999; 99FR-0003925.  
XX  
PA (MERI-) MERISTEM THERAPEUTICS.  
PI Rance I, Gruber V, Theisen M;  
XX  
XX WPI; 2000-647238/62.  
DR  
XX  
PT Chimeric expression promoter for transgenic plant production, comprises  
PT sequence from promoter comprising vascular expression region replaced  
PT with sequence from promoter comprising green tissue expression region  
PT  
PS  
XX Claim 5; Page 82; 91pp; English.  
XX  
CC The present sequence represents a chimeric promoter of the invention.  
CC The specification describes chimeric expression promoters. These  
CC chimeric promoters comprise a nucleic acid sequence which is derived  
CC from a first plant promoter, in which a plant vascular expression  
CC promoter region is replaced with a nucleic acid sequence derived from  
CC a second plant promoter comprising a plant green tissue expression  
CC promoter region. Preferably, the first plant promoter originates from  
CC cornelina yellow mottle virus, and the second plant promoter originates  
CC from the Cassava vein mosaic virus. Especially, the promoters are  
CC derived from intergenic regions. The chimeric promoters are useful  
CC for producing transgenic plants.  
XX  
SQ Sequence 398 BP; 128 A; 80 C; 93 G; 97 T; 0 other;  
XX  
Query Match 23.5%; Score 140.8; DB 21; Length 398;  
Best Local Similarity 98.1%; Pred. No. 4e-33;  
Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
XX  
QY 78 CATGACACTGTGCGCAATTGTAAGACGTACACTGACGACACATGAAAGAGAA 137  
DB 160 CATGCCACTCTGTGCATATTGTAAGACGTACACTGACGACACATGAAAGAGAA 219  
QY 138 GATAAGTCGCGTATTGTGAAGACATGAGACACATGTAAGTGGPAAAAATGTAAG 197  
DB 220 GATAAGTCGCGTATTGTG- AAGAGACATGAGACACATGTAAGTGGAAAAATGTAAG 278  
QY 198 GCGGAAAGTAACTTATGCAATTTGTAATTTGGTTAC 233  
DB 279 GCGGAAAGTAACTTATGCAATTTGTAATTTGGTTAC 314  
XX  
RESULT 13  
AAV14019  
ID AAV14019 standard; DNA; 392 BP.  
XX  
AC AAV14019;  
XX  
DT 18-JUN-1998 (first entry)  
XX  
DE CSMV promoter CVP1.  
XX  
KM Cassava vein mosaic virus; CSMV; promoter; cultivated crop;  
KM tissue-specific expression control; transgenic plant; ss.  
XX  
OS Cassava vein mosaic virus.  
XX  
PN WO9748819-A1.  
XX  
PD 24-DEC-1997.  
XX  
PF 20-JUN-1997; 97WO-US10376.  
XX  
PR 20-JUN-1996; 96US-0020129.  
XX  
PA (SCRI) SCRIPPS RES INST.  
XX

PI Beachy RN, De Kochko A, Fauquet C, Verdagner B;  
XX  
DR WPI; 1998-063157/06.  
XX  
XX Cassava vein mosaic virus promoter - used to express heterologous  
PT DNA sequences for producing transgenic plants having altered  
PT phenotype(s)  
XX  
PS Claim 2; Page 74; 115pp; English.  
XX  
CC This sequence represents a cassava vein mosaic virus promoter, and  
CC is a nucleic acid molecule of the invention. The promoter is capable of  
CC initiating transcription of an operably linked heterologous nucleic acid  
CC sequence in a plant cell. The CSMV promoters are active in both monocot  
CC and dicot plant species, and therefore can be readily applied to a  
CC variety of cultivated crops. Although generally constitutive, the  
CC derivative promoters include promoters that can regulate expression in a  
CC tissue-specific manner, and therefore are useful for controlling  
CC expression of heterologous genes in a tissue-specific manner. The  
CC promoters can be used for producing transgenic plants with an altered  
CC phenotype.  
XX  
SQ Sequence 392 BP; 154 A; 64 C; 83 G; 91 T; 0 other;  
XX  
Query Match 20.1%; Score 120.6; DB 19; Length 392;  
Best Local Similarity 93.3%; Pred. No. 6.2e-27;  
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
XX  
QY 93 GAATATTGAAGACGTAAAGCACTGACGACACATGTAAGAAAGACATTAAGTCGCTGAT 152  
DB 143 GAATCTTGAAGACGTAAAGCACTGACGACACATGTAAGAAAGACATTAAGTCGCTGAT 202  
QY 153 TGTGAAGAGACATGAGACACATGTAAGGTGGAATGTGAAGCGCGAAAGTAACTTT 212  
DB 203 TGTGAAGAGACATGAGACACATGTAAGGTGGAATGTGAAGCGCGAAAGTAACTTT 262  
QY 213 ATGCAATTTGTAATTT 227  
DB 263 ATCACAAGGAATCT 277  
XX  
RESULT 14  
AAV14021  
ID AAV14021 standard; DNA; 411 BP.  
XX  
AC AAV14021;  
XX  
DT 18-JUN-1998 (first entry)  
XX  
DE CSMV promoter pB.  
XX  
KM Cassava vein mosaic virus; CSMV; promoter; cultivated crop;  
KM tissue-specific expression control; transgenic plant; ss.  
XX  
OS Cassava vein mosaic virus.  
XX  
PN WO9748819-A1.  
XX  
PD 24-DEC-1997.  
XX  
PF 20-JUN-1997; 97WO-US10376.  
XX  
PR 20-JUN-1996; 96US-0020129.  
XX  
PA (SCRI) SCRIPPS RES INST.  
XX  
PI Beachy RN, De Kochko A, Fauquet C, Verdagner B;  
XX  
DR WPI; 1998-063157/06.  
XX  
XX Cassava vein mosaic virus promoter - used to express heterologous  
PT DNA sequences for producing transgenic plants having altered  
PT phenotype(s)  
XX

XX Claim 2; Page 76-77; 115pp: English.  
PS  
XX This sequence represents a cassava vein mosaic virus promoter, and  
CC is a nucleic acid molecule of the invention. The promoter is capable of  
CC initiating transcription of an operably linked heterologous nucleic acid  
CC sequence in a plant cell. The CaMV promoters are active in both monocot  
CC and dicot plant species, and therefore can be readily applied to a  
CC variety of cultivated crops. Although generally constitutive, the  
CC derivative promoters include promoters that can regulate expression in a  
CC tissue-specific manner, and therefore are useful for controlling  
CC expression of heterologous genes in a tissue-specific manner. The  
CC promoters can be used for producing transgenic plants with an altered  
CC phenotype.  
XX  
SQ Sequence 411 BP; 157 A; 60 C; 87 G; 107 T; 0 other;  
Query Match 20.1%; Score 120.6; DB 19; Length 411;  
Best Local Similarity 93.3%; Pred. No. 6.3e-27;  
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 93 GAATATTGAAGACGTAAGCACTGACGACACATGAAAGAAAGATAGGTGCGTAT 152  
DB 107 GAATCTTGAAGACGTAAGCACTGACGACACATGAAAGAAAGATAGGTGCGTAT 166  
QY 153 TGTGAAGAGACATAGAGGACACATGTAAGGTGGAATGTAAGGCGCGAAAGTAACCTT 212  
DB 167 TGTGAAGAGACATAGAGGACACATGTAAGGTGGAATGTAAGGCGCGAAAGTAACCTT 226  
QY 213 ATGCATTGTAAATTT 227  
DB 227 ATCACAAGGAATCT 241

RESULT 15  
ID AAA96836  
AC AAA96836;  
DT 19-FEB-2001 (first entry)  
DE Promoter from intergenic region of Cassava vein mosaic virus.  
KW Promoter; intergenic region; Commelina yellow mottle virus;  
KW chimeric expression promoter; plant vascular expression promoter;  
KW plant green tissue expression promoter; Cassava vein mosaic virus;  
KW transgenic plant; ss.  
XX  
XX Cassava vein mosaic virus.  
XX OS  
XX PN W0200058485-A1.  
XX PD 05-OCT-2000.  
XX PF 29-MAR-2000; 2000WO-1B00370.  
XX PR 29-MAR-1999; 99FR-0003925.  
XX PA (MERI-) MERISTEM THERAPEUTICS.  
XX PI Rance I, Gruber V, Theisen M;  
XX WPI: 2000-647238/62.  
XX  
XX Chimeric expression promoter for transgenic plant production, comprises  
PT sequence from promoter comprising vascular expression region replaced  
PT with sequence from promoter comprising green tissue expression region  
PT  
XX  
XX Claim 4; Page 80; 91pp: English.  
XX  
XX The present sequence represents a promoter fragment from the intergenic

CC region of Cassava vein mosaic virus. The promoter is used to construct  
CC chimeric expression promoters. These chimeric promoters comprise a  
CC nucleic acid sequence which is derived from a first plant promoter,  
CC in which a plant vascular expression promoter region is replaced with  
CC a nucleic acid sequence derived from a second plant promoter comprising  
CC a plant green tissue expression promoter region. Preferably, the first  
CC plant promoter originates from commelina yellow mottle virus, and the  
CC second plant promoter originates from the Cassava vein mosaic virus.  
CC The chimeric promoters are useful for producing transgenic plants.  
XX  
SQ Sequence 515 BP; 198 A; 79 C; 109 G; 129 T; 0 other;  
Query Match 20.1%; Score 120.6; DB 21; Length 515;  
Best Local Similarity 93.3%; Pred. No. 6.9e-27;  
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 93 GAATATTGAAGACGTAAGCACTGACGACACATGAAAGAAAGATAGGTGCGTAT 152  
DB 216 GAATCTTGAAGACGTAAGCACTGACGACACATGAAAGAAAGATAGGTGCGTAT 275  
QY 153 TGTGAAGAGACATAGAGGACACATGTAAGGTGGAATGTAAGGCGCGAAAGTAACCTT 212  
DB 276 TGTGAAGAGACATAGAGGACACATGTAAGGTGGAATGTAAGGCGCGAAAGTAACCTT 335  
QY 213 ATGCATTGTAAATTT 227  
DB 336 ATCACAAGGAATCT 350

Search completed: April 14, 2003, 08:19:41  
Job time : 196.814 secs



GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 08:01:47 ; Search time 61.8557 Seconds  
(without alignments)  
2974.765 Million cell updates/sec

Title: US-09-963-803-22

Perfect score: 600

Sequence: 1 aagcttgctgcctgcagca.....cacacaactagagatcc 600

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/1/lna/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/lna/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/lna/5A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/lna/5B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/lna/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/lna/backfile1.esl.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description                         |
|------------|-------|-------------|--------|-------|-------------------------------------|
| C 1        | 54.8  | 9.1         | 7218   | 1     | US-08-232-463-14 Sequence 14, Appl  |
| 2          | 40.4  | 6.7         | 439    | 1     | US-08-247-809A-3 Sequence 3, Appl   |
| 3          | 40.4  | 6.7         | 439    | 2     | US-08-711-728-3 Sequence 3, Appl    |
| 4          | 40.4  | 6.7         | 446    | 1     | US-08-764-100-23 Sequence 23, Appl  |
| 5          | 40.4  | 6.7         | 532    | 3     | US-09-042-426-1 Sequence 1, Appl    |
| 6          | 40.4  | 6.7         | 532    | 4     | US-09-291-238-1 Sequence 1, Appl    |
| 7          | 40.4  | 6.7         | 532    | 4     | US-09-330-760-1 Sequence 1, Appl    |
| 8          | 40.4  | 6.7         | 532    | 4     | US-09-328-473-1 Sequence 1, Appl    |
| 9          | 40.4  | 6.7         | 532    | 4     | US-09-330-737-1 Sequence 1, Appl    |
| 10         | 40.4  | 6.7         | 532    | 4     | US-09-329-169-1 Sequence 1, Appl    |
| 11         | 40.4  | 6.7         | 532    | 4     | US-09-330-714A-1 Sequence 1, Appl   |
| 12         | 40.4  | 6.7         | 532    | 4     | US-09-328-826-1 Sequence 1, Appl    |
| 13         | 40.4  | 6.7         | 560    | 3     | US-09-042-426-5 Sequence 5, Appl    |
| 14         | 40.4  | 6.7         | 560    | 4     | US-09-291-238-5 Sequence 5, Appl    |
| 15         | 40.4  | 6.7         | 560    | 4     | US-09-330-760-5 Sequence 5, Appl    |
| 16         | 40.4  | 6.7         | 560    | 4     | US-09-328-473-5 Sequence 5, Appl    |
| 17         | 40.4  | 6.7         | 560    | 4     | US-09-330-737-5 Sequence 5, Appl    |
| 18         | 40.4  | 6.7         | 560    | 4     | US-09-329-169-5 Sequence 5, Appl    |
| 19         | 40.4  | 6.7         | 560    | 4     | US-09-330-714A-5 Sequence 5, Appl   |
| 20         | 40.4  | 6.7         | 560    | 4     | US-09-328-826-5 Sequence 5, Appl    |
| 21         | 40.4  | 6.7         | 661    | 4     | US-09-027-998A-33 Sequence 33, Appl |
| 22         | 40.4  | 6.7         | 793    | 4     | US-08-371-764-1 Sequence 1, Appl    |
| 23         | 40.4  | 6.7         | 793    | 4     | US-08-897-736-1 Sequence 1, Appl    |
| 24         | 40.4  | 6.7         | 831    | 1     | US-08-450-834-5 Sequence 5, Appl    |
| 25         | 40.4  | 6.7         | 950    | 6     | 5177308-3 Patent No. 5177308        |
| 26         | 40.4  | 6.7         | 978    | 1     | US-08-446-486-31 Sequence 31, Appl  |
| 27         | 40.4  | 6.7         | 978    | 1     | US-08-463-308-31 Sequence 31, Appl  |

|    |      |     |      |   |                                     |
|----|------|-----|------|---|-------------------------------------|
| 28 | 40.4 | 6.7 | 979  | 1 | US-08-446-486-30 Sequence 30, Appl  |
| 29 | 40.4 | 6.7 | 979  | 1 | US-08-463-308-30 Patent No. 5254799 |
| 30 | 40.4 | 6.7 | 980  | 6 | 5254799-30 Sequence 46, Appl        |
| 31 | 40.4 | 6.7 | 1030 | 1 | US-07-936-163-46 Sequence 43, Appl  |
| 32 | 40.4 | 6.7 | 1030 | 4 | US-08-729-601A-43 Sequence 35, Appl |
| 33 | 40.4 | 6.7 | 1034 | 4 | US-09-363-970-35 Sequence 8, Appl   |
| 34 | 40.4 | 6.7 | 1138 | 4 | US-09-011-151-8 Sequence 9, Appl    |
| 35 | 40.4 | 6.7 | 1138 | 4 | US-09-011-151-9 Sequence 9, Appl    |
| 36 | 40.4 | 6.7 | 1196 | 4 | US-08-729-601A-46 Sequence 2, Appl  |
| 37 | 40.4 | 6.7 | 1279 | 4 | US-09-185-244-2 Sequence 2, Appl    |
| 38 | 40.4 | 6.7 | 1279 | 4 | US-09-471-913-6 Sequence 6, Appl    |
| 39 | 40.4 | 6.7 | 1303 | 3 | US-08-894-440-2 Sequence 2, Appl    |
| 40 | 40.4 | 6.7 | 1303 | 4 | US-09-458-093-2 Sequence 2, Appl    |
| 41 | 40.4 | 6.7 | 1651 | 3 | US-09-065-999-5 Sequence 5, Appl    |
| 42 | 40.4 | 6.7 | 1651 | 3 | US-09-065-999-6 Sequence 6, Appl    |
| 43 | 40.4 | 6.7 | 1722 | 1 | US-08-247-809A-5 Sequence 5, Appl   |
| 44 | 40.4 | 6.7 | 1722 | 2 | US-08-711-728-5 Sequence 5, Appl    |
| 45 | 40.4 | 6.7 | 1829 | 1 | US-07-966-187-17 Sequence 17, Appl  |

#### ALIGNMENTS

RESULT 1  
US-08-232-463-14/C  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,463  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935,313  
; FILING DATE:  
; APPLICATION NUMBER: 26-AUG-1991  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)836-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7218 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: PT99pt-F1s  
; US-08-232-463-14  
Query Match 9.1% Score 54.8; DB 1; Length 7218;

Best Local Similarity 6.3%; Pred. No. 3.4e-07;  
Matches 26; Conservative 216; Mismatches 168; Indels 0; Gaps 0;

OY 66 TGAATAGCAGCCAGCCTGTGCGAATATGTAAGCACTAGACAGACAGACA 125  
DB 1482 TAATTACCACTATTGTCAGTGTAAAGATAGAAATTTGTCACRRRRRRRR 1423  
OY 126 TGAAGAAGAGATAGAGTCGGTGTGTGAAGACATAGACACATGAAGTG 185  
DB 1422 RRR 1363  
OY 186 GAAATGTAGCGCGAAGTAACCTTATGATTTGTAATTGGTTACGATGATG 245  
DB 1362 RRR 1303  
OY 246 ATGTGATTCAGATTGATGTATCTCCACTGACGTAGGAGGACCAAGCAGC 305  
DB 1302 RRR 1243  
OY 306 TAGTATGATGTATATCAAGATTGATGTATCTCCACTGACGTAGGAGCAGCA 365  
DB 1242 RRR 1183  
OY 366 TGCCACGACTAGTGTATGTATCAAGATTGATGTATCTCCACTGACGTAGG 425  
DB 1182 RRR 1123  
OY 426 GATGACGATGCCAGCTAGTGTATGTATCAAGATTGATGTA 475  
DB 1122 RRR 1073

## RESULT 2

US-08-247-809A-3  
Sequence 3, Application US/08247809A  
Patent No. 5569823  
GENERAL INFORMATION:  
APPLICANT: Peter H. Schreier; Klaus Stenzel; Gunter Adam;  
APPLICANT: Edgar Maiss  
TITLE OF INVENTION: DEOXYRIBONUCLEIC ACIDS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SPRUNG HORN KRAMER & WOODS  
STREET: 660 White Plains Road  
CITY: Tarrytown  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10591-5144  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB  
MEDIUM TYPE: storage  
COMPUTER: NEC Powermate 1 Plus  
OPERATING SYSTEM: DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/247, 809A  
FILING DATE: May 23, 1994  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: P 43 178 45.6 (Germany)  
FILING DATE: May 28, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kurt G. Briscoe  
REGISTRATION NUMBER: 33,141  
REFERENCE/DOCKET NUMBER: Bayer 9049-KGB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (914) 332-1700  
TELEFAX: (914) 332-1844  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 439 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-247-809A-3

Query Match  
Best Local Similarity 6.7%; Score 40.4; DB 1; Length 439;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 396 GATTGATGTATATCTCCAGCTAGCAATGAGATGACGATGCGACGACTA 445  
DB 338 GATTGATGTATATCTCCAGCTAGCAATGAGATGAGATGACGATGCGAC 387

## RESULT 3

US-08-711-728-3  
Sequence 3, Application US/08711728  
Patent No. 5973135  
GENERAL INFORMATION:  
APPLICANT: Peter H. Schreier; Klaus Stenzel; Gunter Adam;  
APPLICANT: Edgar Maiss  
TITLE OF INVENTION: DEOXYRIBONUCLEIC ACIDS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SPRUNG HORN KRAMER & WOODS  
STREET: 660 White Plains Road  
CITY: Tarrytown  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10591-5144  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB  
MEDIUM TYPE: storage  
COMPUTER: NEC Powermate 1 Plus  
OPERATING SYSTEM: DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/711,728  
FILING DATE: 03-SEPT-1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/247, 809  
FILING DATE: 23-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 43178456  
FILING DATE: 28-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kurt G. Briscoe  
REGISTRATION NUMBER: 33,141  
REFERENCE/DOCKET NUMBER: Bayer 9049.1-KGB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (914) 332-1700  
TELEFAX: (914) 332-1844  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 439 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-711-728-3

Query Match  
Best Local Similarity 6.7%; Score 40.4; DB 2; Length 439;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 396 GATTGATGTATATCTCCAGCTAGCAATGAGATGACGATGCGACGACTA 445  
DB 338 GATTGATGTATATCTCCAGCTAGCAATGAGATGAGATGACGATGCGAC 387

## RESULT 4



US-08-764-100-23  
; Sequence 23, Application US/08764100  
; Patent No. 5773700  
; GENERAL INFORMATION:  
; APPLICANT: van Grinsven J., Martinus Q.  
; APPLICANT: De Haan, Petrus T.  
; APPLICANT: Giesen L., Johannes J.  
; APPLICANT: Peters, Dirk  
; APPLICANT: Goldbach, Robert W.  
; TITLE OF INVENTION: Improvements in or Relating to Organic  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sandoz Agro, Inc  
; STREET: 975 California Avenue  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/764,100  
; FILING DATE: 06-DEC-1996  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/214,064  
; FILING DATE:  
; APPLICATION NUMBER: US 08/032,235  
; FILING DATE: 17-MAR-1993  
; APPLICATION NUMBER: GB 9206016.9  
; FILING DATE: 19-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5773700r1s, Allen E.  
; REGISTRATION NUMBER: 34,490  
; REFERENCE/DOCKET NUMBER: 137-1061  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 354-3592  
; TELEFAX: (415) 857-1125  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 446 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-764-100-23  
  
Query Match 6.7%; Score 40.4; DB 1; Length 446;  
Best Local Similarity 88.0%; Pred. No. 0.0028;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

ZIP: 07901  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/042,426  
; FILING DATE: March 13, 1998  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoxie, Thomas  
; REGISTRATION NUMBER: 32,993  
; REFERENCE/DOCKET NUMBER: 135/1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919) 541-8614  
; TELEFAX: (919) 541-8689  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 532 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; IMMEDIATE SOURCE:  
; CLONE: 35S Promoter  
; US-09-042-426-1  
  
Query Match 6.7%; Score 40.4; DB 3; Length 532;  
Best Local Similarity 88.0%; Pred. No. 0.003;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

US-09-291-238-1  
; Sequence 1, Application US/09291238  
; Patent No. 6222104  
; GENERAL INFORMATION:  
; APPLICANT: Irvan J. Mettler, Paul S. Dietrich, Ralph Sinibaldi  
; TITLE OF INVENTION: DNA Construct Containing Bacillus  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6222104artis Corporation  
; STREET: 564 Morris Avenue  
; CITY: Summit  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07901  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/291,238  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/042,426  
; FILING DATE: March 13, 1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoxie, Thomas  
; REGISTRATION NUMBER: 32,993  
; REFERENCE/DOCKET NUMBER: 135/1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919) 541-8614  
; TELEFAX: (919) 541-8689

; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 532 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; IMMEDIATE SOURCE:  
; CLONE: 35S Promoter  
US-09-291-238-1

Query Match 6.7%; Score 40.4; DB 4; Length 532;  
Best Local Similarity 88.0%; Pred. No. 0.003;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 327 GATTGATGATATCTCCACTGACGTAAAGGATGACCATGCCACACTA 376  
DB 274 GATTGATGATATCTCCACTGACGTAAAGGATGACCATGCCACACTA 323

## RESULT 7

US-09-330-760-1  
; Sequence 1, Application US/09330760  
; Patent No. 6229075  
; GENERAL INFORMATION:  
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi  
; TITLE OF INVENTION: DNA Construct Containing Bacillus  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6229075artis Corporation  
; STREET: 564 Morris Avenue  
; CITY: Summit  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07901  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/330,760  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/042,426  
; FILING DATE: March 13, 1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoxie, Thomas  
; REGISTRATION NUMBER: 32,993  
; REFERENCE/DOCKET NUMBER: 135/1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919) 541-8614  
; TELEFAX: (919) 541-8689  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 532 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; IMMEDIATE SOURCE:  
; CLONE: 35S Promoter  
US-09-330-760-1

Query Match 6.7%; Score 40.4; DB 4; Length 532;  
Best Local Similarity 88.0%; Pred. No. 0.003;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 327 GATTGATGATATCTCCACTGACGTAAAGGATGACCATGCCACACTA 376  
DB 274 GATTGATGATATCTCCACTGACGTAAAGGATGACCATGCCACACTA 323

## RESULT 8

US-09-328-473-1  
; Sequence 1, Application US/09328473  
; Patent No. 6232533  
; GENERAL INFORMATION:  
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi  
; TITLE OF INVENTION: DNA Construct Containing Bacillus  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6232534artis Corporation  
; STREET: 564 Morris Avenue  
; CITY: Summit  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07901  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/328,473  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/042,426  
; FILING DATE: March 13, 1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoxie, Thomas  
; REGISTRATION NUMBER: 32,993  
; REFERENCE/DOCKET NUMBER: 135/1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919) 541-8614  
; TELEFAX: (919) 541-8689  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 532 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; IMMEDIATE SOURCE:  
; CLONE: 35S Promoter  
US-09-328-473-1

Query Match 6.7%; Score 40.4; DB 4; Length 532;  
Best Local Similarity 88.0%; Pred. No. 0.003;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 327 GATTGATGATATCTCCACTGACGTAAAGGATGACCATGCCACACTA 376  
DB 274 GATTGATGATATCTCCACTGACGTAAAGGATGACCATGCCACACTA 323

RESULT 9

US-09-330-737-1  
; Sequence 1, Application US/09330737  
; Patent No. 6232534  
; GENERAL INFORMATION:  
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi  
; TITLE OF INVENTION: DNA Construct Containing Bacillus  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6232534artis Corporation  
; STREET: 564 Morris Avenue  
; CITY: Summit

STATE: New Jersey  
COUNTRY: USA  
ZIP: 07901  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/330,737  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,426  
FILING DATE: March 13, 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoxie, Thomas  
REGISTRATION NUMBER: 32,993  
REFERENCE/DOCKET NUMBER: 135/1  
TELEPHONE: (919) 541-8614  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 532 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: 35S Promoter  
US-09-330-737-1

Query Match  
Best Local Similarity 6.7%; Score 40.4; DB 4; Length 532;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 327 GATTGATGATATCTCCACTGACGTAAGGATGACCGATCCACGACTA 376  
274 GATTGATGATATCTCCACTGACGTAAGGATGACCGACATCCACTA 323

RESULT 10  
US-09-329-169-1  
Sequence 1, Application US/09329169  
Patent No. 6329575  
GENERAL INFORMATION:  
APPLICANT: Irvn J. Mettler, Paul S. Dietrich, Ralph Sinibaldi  
TITLE OF INVENTION: DNA Construct Containing Bacillus  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6329575artis Corporation  
STREET: 564 Morris Avenue  
CITY: Summit  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07901  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/329,169  
FILING DATE: 09-Jun-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/042,426  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoxie, Thomas

REGISTRATION NUMBER: 32,993  
REFERENCE/DOCKET NUMBER: 135/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8614  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 532 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: 35S Promoter  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-329-169-1

Query Match  
Best Local Similarity 6.7%; Score 40.4; DB 4; Length 532;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 327 GATTGATGATATCTCCACTGACGTAAGGATGACCGATCCACGACTA 376  
274 GATTGATGATATCTCCACTGACGTAAGGATGACCGACATCCACTA 323

RESULT 11  
US-09-330-714A-1  
Sequence 1, Application US/09330714A  
Patent No. 6342660  
GENERAL INFORMATION:  
APPLICANT: Irvn J. Mettler, Paul S. Dietrich, Ralph Sinibaldi  
TITLE OF INVENTION: DNA Construct Containing Bacillus  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6342660artis Corporation  
STREET: 564 Morris Avenue  
CITY: Summit  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07901  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/330,714A  
FILING DATE: 11-Jun-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/042,426  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoxie, Thomas  
REGISTRATION NUMBER: 32,993  
REFERENCE/DOCKET NUMBER: 135/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8614  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 532 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:

```
; CLONE: 35S Promoter
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-330-714A-1

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 4; Length 532;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 327 GATTGATGATATCTCCACTGACGTAGGATGACGATGCCAGACTA 376
DB 274 GATTGATGATATCTCCACTGACGTAGGATGACGATGCCAGACTA 323

RESULT 12
US-09-328-826-1
; Sequence 1, Application US/09328826
; Patent No. 6399860
; GENERAL INFORMATION:
; APPLICANT: Irvln J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 6399860artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/328,826
; FILING DATE: 09-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,426
; FILING DATE: March 13, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoxie, Thomas
; REGISTRATION NUMBER: 32,993
; REFERENCE/DOCKET NUMBER: 135/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: 35S Promoter
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-328-826-1

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 4; Length 532;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
; Patent No. 6114608
; GENERAL INFORMATION:
; APPLICANT: Irvln J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 6114608artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,426
; FILING DATE: March 13, 1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoxie, Thomas
; REGISTRATION NUMBER: 32,993
; REFERENCE/DOCKET NUMBER: 135/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: 35S Promoter
US-09-042-426-5

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 3; Length 560;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 327 GATTGATGATATCTCCACTGACGTAGGATGACGATGCCAGACTA 376
DB 322 GATTGATGATATCTCCACTGACGTAGGATGACGATGCCAGACTA 371

RESULT 14
US-09-291-238-5
; Sequence 5, Application US/09291238
; Patent No. 6222104
; GENERAL INFORMATION:
; APPLICANT: Irvln J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 6222104artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/291,238
; FILING DATE:
```

```

: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/042,426
: FILING DATE: March 13, 1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Hoxie, Thomas
: REGISTRATION NUMBER: 32,993
: REFERENCE/DOCKET NUMBER: 135/1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 541-8614
: TELEFAX: (919) 541-8689
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 560 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEetical: NO
: ANTI-SENSE: NO
: IMMEDIATE SOURCE:
: CLONE: 35S Promoter
: US-09-291-238-5

Query Match          6.7%; Score 40.4; DB 4; Length 560;
Best Local Similarity 88.0%; Pred. No. 0.0031;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 322 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCAGACTA 376
    |||||||||||||||||||||||||||||||||||||||
Db 322 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCAGACTA 371

RESULT 15
US-09-330-760-5
: Sequence 5, Application US/09330760
: Patent No. 6229075
: GENERAL INFORMATION:
: APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
: TITLE OF INVENTION: DNA Construct Containing Bacillus
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 6229075artis Corporation
: STREET: 564 Morris Avenue
: City: Summit
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07901
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/330,760
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/042,426
: FILING DATE: March 13, 1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Hoxie, Thomas
: REGISTRATION NUMBER: 32,993
: REFERENCE/DOCKET NUMBER: 135/1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 541-8614
: TELEFAX: (919) 541-8689
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 560 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear

```

```

: MOLECULE TYPE: DNA (genomic)
: HYPOTHEtical: NO
: ANTI-SENSE: NO
: IMMEDIATE SOURCE:
: CLONE: 35S Promoter
: US-09-330-760-5

Query Match          6.7%; Score 40.4; DB 4; Length 560;
Best Local Similarity 88.0%; Pred. No. 0.0031;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 322 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCAGACTA 376
    |||||||||||||||||||||||||||||||||||||||
Db 322 GATTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCAGACTA 371

Search completed: April 14, 2003, 10:28:42
Job time : 67.8557 secs

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Db 121 AACATGAAAGAGAAAGTAAGTGGGTGATTGTGAAAGAGACATAGAGACACATGTA 180
Qy 181 AGGTGAAAAATGTAAGGGCGGAAAGTAACCTTATGCAATTTGGTTACGACTAGT 240
Db 181 AGGTGAAAAATGTAAGGGCGGAAAGTAACCTTATGCAATTTGGTTACGACTAGT 240
Qy 241 GATTGATGATATCAAGATTGATGATATCCACTAGCTAAGGGATGAGCGCTAGC 300
Db 241 GATTGATGATATCAAGATTGATGATATCCACTAGCTAAGGGATGAGCGCTAGC 300
Qy 301 ACGACTAGTATGATGATATCAAGATTGATGATATCCACTAGCTAAGGGATG 360
Db 301 ACGACTAGTATGATGATATCAAGATTGATGATATCCACTAGCTAAGGGATG 360
Qy 361 ACGCATGCCACGACTAGTATGATGATATCCACTAGCTAAGGGATG 420
Db 361 ACGCATGCCACGACTAGTATGATGATATCCACTAGCTAAGGGATG 420
Qy 421 TAAGGATGACGATGACGACGACTAGTATGATGATATCCACTAGCTAAGGGATG 480
Db 421 TAAGGATGACGATGACGACGACTAGTATGATGATATCCACTAGCTAAGGGATG 480
Qy 481 CCACTGACGTAAGGATGACGACGACTAGTATCCCGGTATGCCGCTTAT 540
Db 481 CCACTGACGTAAGGATGACGACGACTAGTATCCCGGTATGCCGCTTAT 540
Qy 541 TTCCTATTATTAAGCACTTGTGTAGTGTAGTAAACCAACAACTAGAGATGC 600
Db 541 TTCCTATTATTAAGCACTTGTGTAGTGTAGTAAACCAACAACTAGAGATGC 600
```

## RESULT 2

```
US-09-963-803-20
; Sequence 20, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963, 803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPr1163
; NAME/KEY: promoter
; LOCATION: (1)..(462)
; OTHER INFORMATION:
US-09-963-803-20
```

```
Query Match 62.3%; Score 373.6; DB 9; Length 462;
Best Local Similarity 95.3%; Pred. No. 2e-102;
Matches 385; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
```

```
Qy 1 AAGCTTGCAATGCGCTGAGACAGTATGCGCGCTCATCATGACATCAGACAGTCTGA 60
Db 1 AAGCTTGCAATGCGCTGAGACAGTATGCGCGCTCATCATGACATCAGACAGTCTGA 60
Qy 61 GGAGATGATAGTACGACAGTCTGTCGCAATATTGAAGAGCTAAGACGCTGACGAC 120
Db 61 GGAGATGATAGTACGACAGTCTGTCGCAATATTGAAGAGCTAAGACGCTGACGAC 120
```

```
Qy 121 AACATGAAAGAGAAAGTAAGTGGGTGATTGTGAAAGAGACATAGAGACACATGTA 180
Db 121 AACATGAAAGAGAAAGTAAGTGGGTGATTGTGAAAGAGACATAGAGACACATGTA 180
Qy 181 AGGTGAAAAATGTAAGGGCGGAAAGTAACCTTATGCAATTTGGTTACGACTAGT 240
Db 181 AGGTGAAAAATGTAAGGGCGGAAAGTAACCTTATGCAATTTGGTTACGACTAGT 240
Qy 241 GATTGATGATATCAAGATTGATGATATCCACTAGCTAAGGGATGAGCGCTAGC 300
Db 241 GATTGATGATATCAAGATTGATGATATCCACTAGCTAAGGGATGAGCGCTAGC 300
Qy 301 ACGACTAGTATGATGATATCAAGATTGATGATATCCACTAGCTAAGGGATG 360
Db 301 ACGACTAGTATGATGATATCAAGATTGATGATATCCACTAGCTAAGGGATG 360
Qy 361 ACGCATGCCACGACTAGTATGATGATATCCACTAGCTAAGGGATG 404
Db 361 ACGCATGCCACGACTAGTATGATGATATCCACTAGCTAAGGGATG 404
```

## RESULT 3

```
US-09-963-803-23
; Sequence 23, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963, 803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 604
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPr1167
; NAME/KEY: promoter
; LOCATION: (1)..(604)
; OTHER INFORMATION:
US-09-963-803-23
```

```
Query Match 52.0%; Score 312.2; DB 9; Length 604;
Best Local Similarity 84.5%; Pred. No. 6.1e-84;
Matches 442; Conservative 0; Mismatches 3; Indels 78; Gaps 5;
```

```
Qy 78 CATGACACTCTGTGCGAATATTGAAGAGCTAAGCACTGACGCAACAATGAAAGAAAGA 137
Db 160 CATGCCACTCTGTGCGAATATTGAAGAGCTAAGCACTGACGCAACAATGAAAGAAAGA 219
Qy 138 GATTAAGTGGGTGATGTAAGAGACATAGAGGACACATGTAAGCTGAAAAATTAAG 197
Db 220 GATTAAGTGGGTGATGTAAGAGACATAGAGGACACATGTAAGCTGAAAAATTAAG 278
Qy 198 GCGGAAAGTAACCTTATGCAATTTGGTTACGACTAGTATGATGATATCA 257
Db 279 GCGGAAAGTAACCTTATGCAATTTGGTTACGACTAGTATGATGATATCA 314
Qy 258 GATTGATGATATCTCAGCTAGCTAAGGGATGAGCGATGCCAGCTAGTATGATG 317
Db 315 -----CTAGTATGATG 327
Qy 318 TGATATCAAGATTGATGATATCTCAGCTAGCTAAGGGATGAGCGATGCCAGCTAG 377
Db 328 TGATATCAAGATTGATGATATCTCAGCTAGCTAAGGGATGAGCGATGCCAGCTAG 385
```



|    |     |  |     |
|----|-----|--|-----|
| QY | 378 | TGATTGATGCAATTCGAAGTATGATGATATCTCCACTACGTAACGTAAGGATGACGCAATGC | 437 |
| Db | 386 | TGATTGATGCAATTCGAAGTATGATGATATCTCCACTACGTAACGTAAGGATGACGCAATGC | 445 |
| QY | 438 | CACGACATAGTATGATGATGATATCAAGATGATGATATATCTCCACTGACGTAAAGGAT    | 497 |
| Db | 446 | CAC--CTAGGATGATGATGATATCAAGATGATGATATATCTCCACTGACGTAAAGGAT     | 503 |
| QY | 498 | GAGCGATGCCAGTTACCCGGTATGCCGGTTCACAGCTTATTTCTTATTTAAGCACT       | 557 |
| Db | 504 | GACCAATGCCAGTTACCCGGTATGCTGGTTCACAGCTTATTTCTTATTTAA--ACT       | 561 |
| QY | 558 | TGTGTAGTACGTTGAAACAACACAACAACCTAGAGGATCC                       | 600 |
| Db | 562 | TGTGTAGTACGTTGAAACAACACAACAACCTAGAGGATCC                       | 604 |

```

RESULT 4
US-09-963-803-19
; Sequence 19, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow r
; TITLE OF INVENTION: vitrus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: PR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ. ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MP1162
; FEATURE:
; NAME/KEY: Promoter
; LOCATION: (1)..(393)
; OTHER INFORMATION:
; US-09-963-803-19

```

```

Db      301  ACGTTACCGGATGCGCGTTCCCAAGCTTATT 335

RESULT 5
US-09-963-803-24
: Sequence 24, Application US/09963803
: Publication No. US20030028922A1
: GENERAL INFORMATION:
: APPLICANT: Meristem Therapeutics
: TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
: FILE REFERENCE: 184332042
: CURRENT APPLICATION NUMBER: US/09/963,803
: CURRENT FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: FR 99/03925
: PRIOR FILING DATE: 1999-03-29
: PRIOR APPLICATION NUMBER: PCT IB00/00370
: PRIOR FILING DATE: 2000-10-05
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 24
: LENGTH: 541
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: promoter MP1168
: NAME/KEY: promoter
: LOCATION: (1)..(541)
: OTHER INFORMATION:
: US-09-963-803-24

```

RESULT 6  
 US-09-963-803-21  
 : Sequence 21, Application US/09963803  
 : Publication No. US20030028922A1  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: Meristem Therapeutics  
 :  
 : TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellic  
 : TITLE OF INVENTION: Virus and cassava vein mosaic virus  
 : FILE REFERENCE: 184332042  
 :  
 : CURRENT APPLICATION NUMBER: US/09/963,803  
 :  
 : CURRENT FILING DATE: 2001-09-26  
 :  
 : PRIOR APPLICATION NUMBER: FR 99/03925

;; PRIOR FILING DATE: 1999-03-29  
;; PRIOR APPLICATION NUMBER: PCT IB00/00370  
;; PRIOR FILING DATE: 2000-10-05  
;; NUMBER OF SEQ ID NOS: 39  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 21  
;; LENGTH: 392  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: promoter MP11164  
;; NAME/KEY: promoter  
;; LOCATION: (1)..(392)  
;; OTHER INFORMATION:  
US-09-963-803-21

Query Match 39.0%; Score 234.2; DB 9; Length 392;  
Best Local Similarity 96.8%; Pred. No. 1.3e-60;  
Matches 239; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 AACCTTGATGCGCTGAGACTAGTATCCGCCGTCATCAATGACATCATCAGTACTGA 60  
DB 1 AAGCTTGATGCGCTGAGACTAGTATCCGCCGTCATCAATGACATCATCAGTACTGA 60  
OY 61 GGAGATGATAGTACCTGACCTGCTGTGCGAATATTGAAGACGTAAAGCAGTACGAC 120  
DB 61 GGAGATGATAGTACCTGACCTGCTGTGCGAATATTGAAGACGTAAAGCAGTACGAC 120  
OY 121 AACATGAAAGAAAGAAAGTAAAGTTCGATTTGAAAGACATAGACATAGTA 180  
DB 121 AACATGAAAGAAAGAAAGTAAAGTTCGATTTGAAAGACATAGACATAGTA 180  
OY 181 AGGTGAAATGTAAAGGCGGAAAGTAACTTATGCAATTTGATTTGATTCAGTACT 240  
DB 181 AGGTGAAATGTAAAGGCGGAAAGTAACTTATGCAATTTGATTTGATTCAGTACT 240  
OY 241 GATTGAT 247  
DB 241 GCGTCAT 247

RESULT 7  
US-09-963-803-3  
; Sequence 3, Application US/09963803  
; Publication No. US20030028922A1  
; GENERAL INFORMATION:  
; APPLICANT: Meristem Therapeutics  
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow  
; FILE REFERENCE: 184332042  
; CURRENT APPLICATION NUMBER: US/09/963,803  
; PRIOR FILING DATE: 1999-03-29  
; PRIOR APPLICATION NUMBER: PCT IB00/00370  
; PRIOR FILING DATE: 2000-10-05  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 317  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Promoter MP1116  
; NAME/KEY: promoter  
; LOCATION: (1)..(317)  
; OTHER INFORMATION:  
US-09-963-803-3

Query Match 35.4%; Score 212.4; DB 9; Length 317;  
Best Local Similarity 99.5%; Pred. No. 4e-54;

Matches 213; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 20 ACTAGTATCCGCGTCATCATGACATCATCAGTACTGAGAGATGATAGTACCA 79  
DB 18 ACTAGTATCCGCGTCATCATGACATCATCAGTACTGAGAGATGATAGTACCA 77  
OY 80 TGACACTGTGCGAATATTGAAGACGTAAAGCAGTACGACACAAATGAAAGAAAGA 139  
DB 78 TGACACTGTGCGAATATTGAAGACGTAAAGCAGTACGACACAAATGAAAGAAAGA 137  
OY 140 TAAGTCGCTGATTTGTAAGAGACATAGAGACATAGTAAAGTGGAAATGTAAGCC 199  
DB 138 TAAGTCGCTGATTTGTAAGAGACATAGAGACATAGTAAAGTGGAAATGTAAGCC 197  
OY 200 GAAAGTAACTTATGCAATTTGTAATTTGTTAC 233  
DB 198 GAAAGTAACTTATGCAATTTGTAATTTGTTAC 231

RESULT 8  
US-09-963-803-25  
; Sequence 25, Application US/09963803  
; Publication No. US20030028922A1  
; GENERAL INFORMATION:  
; APPLICANT: Meristem Therapeutics  
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow  
; FILE REFERENCE: 184332042  
; CURRENT APPLICATION NUMBER: US/09/963,803  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: FR 99/03925  
; PRIOR FILING DATE: 1999-03-29  
; PRIOR APPLICATION NUMBER: PCT IB00/00370  
; PRIOR FILING DATE: 2000-10-05  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 25  
; LENGTH: 472  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: promoter MP1169  
; NAME/KEY: promoter  
; LOCATION: (1)..(472)  
; OTHER INFORMATION:  
US-09-963-803-25

Query Match 35.4%; Score 212.4; DB 9; Length 472;  
Best Local Similarity 91.5%; Pred. No. 4.9e-54;  
Matches 236; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

OY 78 CATGACACTCTGTGCGAATATTGAAGACGTAAAGCAGTACGACAAATGAAAGAAAGA 137  
DB 160 CATGACACTCTGTGCGAATATTGAAGACGTAAAGCAGTACGACAAATGAAAGAAAGA 219  
OY 138 GATGAGTCGCGATTTGTAAGAGACATAGAGACATGATTAAGTGGAAATGTAAGG 197  
DB 220 GATGAGTCGCGATTTGTAAGAGACATAGAGACATGATTAAGTGGAAATGTAAGG 278  
OY 198 GCGGAAAGTAACTTATGCAATTTGTAATTTGTTACGATAGTATGATGATGATCA 257  
DB 279 GCGGAAAGTAACTTATGCAATTTGTAATTTGTTACGATAGTATGATGATGATCA 338  
OY 258 GATTGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 317  
DB 339 GATTGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 398  
OY 318 TGATATCAAGATGATG 335  
DB 399 GGTTCCTCAAGCTTTATTTT 416

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RESULT 9
US-09-963-803-4
; Sequence 4, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPr1117
; NAME/KEY: promoter
; LOCATION: (1)..(348)
; OTHER INFORMATION:
US-09-963-803-4

Query Match          33.4%; Score 200.4; DB 9; Length 348;
Best Local Similarity 99.1%; Pred. No. 1.7e-50;
Matches 212; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 20 ACTAGTATCCCGCTCATCATGATCATCATGAGTACTGAGAGATGATGCTAGCCA 79
    |||||||
DB 52 ACTAGTATCCCGCTCATCATGATCATCATGAGTACTGAGAGATGATGCTAGCCA 111
    |||||||
QY 80 TGACACTCTGTGCGAATATTGAAGACGTAGACACTGACGACAAATGAAAGAAAGA 139
    |||||||
DB 112 TGACACTCTGTGCGAATATTGAAGACGTAGACACTGACGACAAATGAAAGAAAGA 171
    |||||||
QY 140 TAAGTCGGTGATTTGTGAAGACATAGAGACATGTAAAGTGGAAATGTAAAGGC 199
    |||||||
DB 172 TAAGTCGGTGATTTGTG- AAGAGACATPAGAGACACATGTAAAGTGGAAATGTAAAGGC 230
    |||||||
QY 200 GGAAGTAACTTATGCATTGTGTAATTTGGTTAC 233
    |||||||
DB 231 GGAAGTAACTTATGCATTGTGTAATTTGGTTAC 264
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RESULT 10
US-09-963-803-5
; Sequence 5, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 371
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPr1146
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; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(371)
; OTHER INFORMATION:
US-09-963-803-5

Query Match          25.5%; Score 152.8; DB 9; Length 371;
Best Local Similarity 98.7%; Pred. No. 3.4e-36;
Matches 154; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 78 CATGACACTCTGTGCGAATATTGAAGACGTAGACACTGACGACAAATGAAAGAA 137
    |||||||
DB 130 CATGCACTCTGTGCGAATATTGAAGACGTAGACACTGACGACAAATGAAAGAA 189
    |||||||
QY 138 GATAAGTCGGTGATTTGTGAAGACATAGAGACACATGTAAAGTGGAAATGTAAAG 197
    |||||||
DB 190 GATAAGTCGGTGATTTGTGAAGACATAGAGACACATGTAAAGTGGAAATGTAAAG 249
    |||||||
QY 198 GCGGAAGTAACTTATGCATTGTGTAATTTGGTTAC 233
    |||||||
DB 182 GCGGAAGTAACTTATGCATTGTGTAATTTGGTTAC 217
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RESULT 11
US-09-963-803-7
; Sequence 7, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yell
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPr1154
; NAME/KEY: promoter
; LOCATION: (1)..(301)
; OTHER INFORMATION:
US-09-963-803-7

Query Match          23.5%; Score 140.8; DB 9; Length 301;
Best Local Similarity 98.1%; Pred. No. 1.2e-32;
Matches 153; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 78 CATGACACTCTGTGCGAATATTGAAGACGTAGACACTGACGACAAATGAAAGAA 137
    |||||||
DB 63 CATGCCACTCTGTGCGAATATTGAAGACGTAGACACTGACGACAAATGAAAGAA 122
    |||||||
QY 138 GATAAGTCGGTGATTTGTGAAGACATAGAGACACATGTAAAGTGGAAATGTAAAG 197
    |||||||
DB 123 GATAAGTCGGTGATTTGTG- AAGAGACATAGAGACACATGTAAAGTGGAAATGTAAAG 181
    |||||||
QY 198 GCGGAAGTAACTTATGCATTGTGTAATTTGGTTAC 233
    |||||||
DB 182 GCGGAAGTAACTTATGCATTGTGTAATTTGGTTAC 217
    |||||||

RESULT 12
US-09-963-803-6
; Sequence 6, Application US/09963803
; Publication No. US20030028922A1
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GenCore version 5.1.4.p5 4578  
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 08:13:29 ; Search time 2420.62 Seconds

(Without alignments)  
6232.082 Million cell updates/sec

Title: US-09-963-803-22

Perfect score: 600

Sequence: 1 aagcttgcatgcctgcagca.....cacacacactagagatcc 600

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues 49582208

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending-Patents\_NA\_Main:\*

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12: /cgn2\_6/prodata/1/pna/US16.COMB.seq:\*

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14: /cgn2\_6/prodata/1/pna/US18.COMB.seq:\*

15: /cgn2\_6/prodata/1/pna/US19.COMB.seq:\*

16: /cgn2\_6/prodata/1/pna/US20.COMB.seq:\*

17: /cgn2\_6/prodata/1/pna/US21.COMB.seq:\*

18: /cgn2\_6/prodata/1/pna/US22.COMB.seq:\*

19: /cgn2\_6/prodata/1/pna/US23.COMB.seq:\*

20: /cgn2\_6/prodata/1/pna/US24.COMB.seq:\*

21: /cgn2\_6/prodata/1/pna/US25.COMB.seq:\*

22: /cgn2\_6/prodata/1/pna/US26.COMB.seq:\*

23: /cgn2\_6/prodata/1/pna/US27.COMB.seq:\*

24: /cgn2\_6/prodata/1/pna/US28.COMB.seq:\*

25: /cgn2\_6/prodata/1/pna/US29.COMB.seq:\*

26: /cgn2\_6/prodata/1/pna/US30.COMB.seq:\*

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33: /cgn2\_6/prodata/1/pna/US37.COMB.seq:\*

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43: /cgn2\_6/prodata/1/pna/US47.COMB.seq:\*

| Result No. | Score | Query Match | Length | DB ID | Description      |
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| 2          | 373.6 | 62.3        | 462    | 36    | US-09-963-803-20 |
| 3          | 312.2 | 52.0        | 604    | 36    | US-09-963-803-23 |
| 4          | 304.6 | 50.8        | 393    | 36    | US-09-963-803-19 |
| 5          | 281.4 | 46.9        | 341    | 36    | US-09-963-803-24 |
| 6          | 234.2 | 39.0        | 392    | 36    | US-09-963-803-21 |
| 7          | 212.4 | 35.4        | 317    | 36    | US-09-963-803-3  |
| 8          | 212.4 | 35.4        | 472    | 36    | US-09-963-803-25 |
| 9          | 200.4 | 33.4        | 348    | 36    | US-09-963-803-1  |
| 10         | 152.8 | 25.5        | 371    | 36    | US-09-963-803-5  |
| 11         | 140.8 | 23.5        | 301    | 36    | US-09-963-803-7  |
| 12         | 140.8 | 23.5        | 388    | 36    | US-09-963-803-6  |
| 13         | 120.6 | 20.1        | 392    | 1     | PCT-US97-10376-1 |
| 14         | 120.6 | 20.1        | 392    | 1     | PCT-US97-10376-1 |
| 15         | 120.6 | 20.1        | 392    | 16    | US-09-202-838-1  |
| 16         | 120.6 | 20.1        | 392    | 16    | US-09-202-838-1  |
| 17         | 120.6 | 20.1        | 411    | 1     | PCT-US97-10376-4 |
| 18         | 120.6 | 20.1        | 411    | 1     | PCT-US97-10376-4 |
| 19         | 120.6 | 20.1        | 411    | 16    | US-09-202-838-4  |
| 20         | 120.6 | 20.1        | 411    | 16    | US-09-202-838-4  |
| 21         | 120.6 | 20.1        | 515    | 25    | US-09-641-466-1  |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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22 120.6 20.1 515 36 US-09-963-803-2 Sequence 2, Appl1
23 120.6 20.1 524 1 PCT-US97-10376-2 Sequence 2, Appl1
24 120.6 20.1 524 1 PCT-US97-10376A-2 Sequence 2, Appl1
25 120.6 20.1 524 16 US-09-202-838-2 Sequence 2, Appl1
26 120.6 20.1 524 16 US-09-202-838-3 Sequence 2, Appl1
27 120.6 20.1 524 16 US-09-202-838A-2 Sequence 2, Appl1
28 120.6 20.1 524 16 US-09-202-838A-3 Sequence 3, Appl1
29 120.6 20.1 526 16 PCT-US97-10376-3 Sequence 3, Appl1
30 120.6 20.1 532 30 PCT-US97-10376A-3 Sequence 3, Appl1
31 120.6 20.1 532 30 US-09-765-555-1 Sequence 19, Appl1
32 120.6 20.1 838 26 US-09-673-274A-19 Sequence 2, Appl1
33 120.6 20.1 853 25 US-09-641-466-2 Sequence 20, Appl1
34 120.6 20.1 1036 26 US-09-673-274A-20 Sequence 4, Appl1
35 120.6 20.1 8340 32 US-09-847-057-4 Sequence 4, Appl1
36 120.6 20.1 8340 33 US-09-874-926-4 Sequence 5, Appl1
37 120.6 20.1 12241 35 PCT-US01-50638-5 Sequence 5, Appl1
38 120.6 20.1 12241 35 US-09-948-138-4 Sequence 5, Appl1
39 120.6 20.1 12241 38 US-10-033-190-5 Sequence 5, Appl1
40 117.4 19.6 305 1 PCT-US97-10376-5 Sequence 5, Appl1
41 117.4 19.6 305 1 PCT-US97-10376A-5 Sequence 5, Appl1
42 117.4 19.6 305 16 US-09-202-838-5 Sequence 5, Appl1
43 117.4 19.6 305 16 US-09-202-838A-5 Sequence 9, Appl1
44 117.4 19.6 420 1 PCT-US97-10376-9 Sequence 9, Appl1
45 117.4 19.6 420 1 PCT-US97-10376A-9
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## ALIGNMENTS

## RESULT 1

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US-09-963-803-22
; Sequence 22, Application US/09963803
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow n
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter Mpr1165
; NAME/KEY: promoter
; LOCATION: (1)..(600)
; OTHER INFORMATION:
US-09-963-803-22
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Query Match 100.0%; Score 600; DB 36; Length 600;
Best Local Similarity 100.0%; Pred. No. 8,9e-163;
Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AAGCTTGCACTGCTGCAGACACTAGTATCCGCCGTCATCATGACATCATCAGTACTGA 60
DB 1 AAGCTTGCACTGCTGCAGACACTAGTATCCGCCGTCATCATGACATCATCAGTACTGA 60
QY 61 GGAGATGAATAGTACCTGACACTCTGTGGCAATATTGAAGAGCTAAGCACTGACGAC 120
DB 61 GGAGATGAATAGTACCTGACACTCTGTGGCAATATTGAAGAGCTAAGCACTGACGAC 120
QY 121 AACCAATGAAGAAGAAAGTAAGTGGTGGTATTGTGAAGAAGACATAGAGACACATGTA 180
DB 121 AACCAATGAAGAAGAAAGTAAGTGGTGGTATTGTGAAGAAGACATAGAGACACATGTA 180
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QY 181 AGGTGGAANAATGTAAAGCGGGAAGTAACCTTATGCAATTTGTAATTTGGTACGACTACT 240
DB 181 AGGTGGAANAATGTAAAGCGGGAAGTAACCTTATGCAATTTGTAATTTGGTACGACTACT 240
QY 241 GATTGATGTGATATCAAGATTGATGATATCTCCACTACGTAAGGATGACGATGCC 300
DB 241 GATTGATGTGATATCAAGATTGATGATATCTCCACTACGTAAGGATGACGATGCC 300
QY 301 ACAGTACGATGATGATATCAAGATTGATGATATCTCCACTACGTAAGGATGAT 360
DB 301 ACAGTACGATGATGATATCAAGATTGATGATATCTCCACTACGTAAGGATGAT 360
QY 361 ACAGTACGATGATGATATCAAGATTGATGATATCTCCACTACGTAAGGATGAT 420
DB 361 ACAGTACGATGATGATATCAAGATTGATGATATCTCCACTACGTAAGGATGAT 420
QY 421 TAAGGATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 421 TAAGGATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 481 CCACGTGACGTAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 481 CCACGTGACGTAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 541 TTCCCTTATTTAAGCACTTGTGTAGTACTTAGAAGAACACACACACACACCTAGAGATCC 600
DB 541 TTCCCTTATTTAAGCACTTGTGTAGTACTTAGAAGAACACACACACACACCTAGAGATCC 600
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## RESULT 2

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US-09-963-803-20
; Sequence 20, Application US/09963803
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter Mpr1163
; NAME/KEY: promoter
; LOCATION: (1)..(462)
; OTHER INFORMATION:
US-09-963-803-20
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Query Match 62.3%; Score 373.6; DB 36; Length 462;
Best Local Similarity 95.3%; Pred. No. 2,9e-97;
Matches 385; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
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QY 1 AAGCTTGCACTGCTGCAGACACTAGTATCCGCCGTCATCATGACATCATCAGTACTGA 60
DB 1 AAGCTTGCACTGCTGCAGACACTAGTATCCGCCGTCATCATGACATCATCAGTACTGA 60
QY 61 GGAGATGAATAGTACCTGACACTCTGTGGCAATATTGAAGAGCTAAGCACTGACGAC 120
DB 61 GGAGATGAATAGTACCTGACACTCTGTGGCAATATTGAAGAGCTAAGCACTGACGAC 120
QY 121 AACCAATGAAGAAGAAAGTAAGTGGTGGTATTGTGAAGAAGACATAGAGACACATGTA 180
DB 121 AACCAATGAAGAAGAAAGTAAGTGGTGGTATTGTGAAGAAGACATAGAGACACATGTA 180
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; Sequence 24, Application US/09963803

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; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
; TITLE OF INVENTION: virus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 24
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPr1168
; NAME/KEY: promoter
; LOCATION: (1)..(541)
; OTHER INFORMATION:
US-09-963-803-24
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Query Match          46.9%; Score 281.4; DB 36; Length 541;
Best Local Similarity 93.3%; Pred. No. 1.5e-70;
Matches 305; Conservative 0; Mismatches 21; Indels 1; Gaps 1;
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QY 78 CATGACACTCTGCGCAATATGGAAGCACTGACGACACATGAAATGGAAGAA 137
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DB 160 CATGCCACTGTGCGAAATATGGAAGCACTGACGACACATGAAATGGAAGAA 219
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 138 GATAAGCTGCGTATGTGTAAGAGACATGAGACACATGTAAGGTGGAATGTAAG 197
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DB 220 GATAGAGTGGGATGTGTC-AAGAGACATGAGAGACACATGTAAGTGGAAATGTAAG 278
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 198 GCGGAAAGTACCTTATGATTTGTAATTTGGTTACGACTAGTATGATGATATCAA 257
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 279 GCGGAAAGTACCTTATGATTTGTAATTTGGTTACGACTAGTATGATGATATCAA 338
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QY 258 GATTGATGATATCCACTGACGTAGAGGATGACCGCATGCCAGCACTAGTATGATG 317
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 339 GATTGATGATATCTCCACTGACGTAGAGGATGACCGCATGCCAGCACTAGTATGATG 398
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QY 318 TGATATCAAGATGATGATATCTCCACTGACGTAGAGGATGACCGCATGCCAGCACTAG 377
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DB 399 TGATATCAAGATGATGATATCTCCACTGACGTAGAGGATGACCGCATGCCAGCTTACC 458
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 378 TGATTGATGTGATATCAAGATTGATGT 404
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 459 CGGTATGCTGTGCCCAACCTTATTT 485
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RESULT 6
US-09-963-803-21
; Sequence 21, Application US/09963803
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
; TITLE OF INVENTION: virus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 21
; LENGTH: 392
; TYPE: DNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPr1164
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(392)
; OTHER INFORMATION:
US-09-963-803-21
```

```

Query Match          39.0%; Score 234.2; DB 36; Length 392;
Best Local Similarity 96.8%; Pred. No. 6.3e-57;
Matches 239; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```

QY 1 AAGCTTGATGCTGCGACACTAGTATCCGCCGTATCATGATCATCAGTACTGTA 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 AAGCTTGATGCTGCGACACTAGTATCCGCCGTATCATGATCATCAGTACTGTA 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 GGAGATGAATAGTACCTGACCTGTGCGAATATTGAAGAGCTAAGCCTACGAC 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 GGAGATGAATAGTACCTGACCTGTGCGAATATTGAAGAGCTAAGCCTACGAC 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 AACATGAAAGAGAGATAGTGTGCGTATGTAAGACATAGAGACATGTA 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 AACATGAAAGAGAGATAGTGTGCGTATGTAAGACATAGAGACATGTA 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 AGGTGGAATATGTAAGGCGGGAAGTAACTTATGATTTGTAATTTGGTTACGACTAGT 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 AGGTGGAATATGTAAGGCGGGAAGTAACTTATGATTTGTAATTTGGTTACGACTAGT 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 GATTGAT 247
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 241 GCGTCAT 247
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```

RESULT 7
US-09-963-803-3
; Sequence 3, Application US/09963803
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
; TITLE OF INVENTION: virus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 3
; LENGTH: 317
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPr116
; NAME/KEY: promoter
; LOCATION: (1)..(317)
; OTHER INFORMATION:
US-09-963-803-3
```

```

Query Match          35.4%; Score 212.4; DB 36; Length 317;
Best Local Similarity 99.5%; Pred. No. 1.2e-50;
Matches 213; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 20 ACTAGTATCGCGGTCATCATATGACATCATCATGACTAGTACGAGAGATGATGACCA 79
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 18 ACTAGTATCGCGGTCATCATATGACATCATCATGACTAGTACGAGAGATGATGACCA 77
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 80 TGACACTGTGTCGCAATATTTGAAGACGTAAAGCACTGACGACACAAATGAAAGAGAGA 139
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 78 TGACACTGTGTCGCAATATTTGAAGACGTAAAGCACTGACGACACAAATGAAAGAGAGA 137
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```



|    |     |   |     |
|----|-----|---|-----|
| Db | 130 | CATGCCACTCGTGCGAATATTGGAAGACGTAAAGCATGACAGCACCAATGAAAAAGAAGAA | 189 |
| Oy | 138 | GATGAAGTCGGTGATTTTGGAAAGACATAGAGACACATGTAAAGTGGAAAAATGTAAAG   | 197 |
| Db | 190 | GATAAGCTCGGTGATTGTGGAAAGACACTAAGACACACTTAAGTGGAAAATGTAAAG     | 249 |
| Oy | 198 | GGCGAAAGTAACTTAGTCATTGTAAATTTGGTTAC                           | 233 |
| Db | 250 | GGCGAAAGTAACTTAGTCATTGTAACTGGTTAC                             | 285 |

```

: RESULT 11
: US-09-963-803-7
: Sequence 7, Application US/09963803
: GENERAL INFORMATION:
: APPLICANT: Meristem Therapeutics
: TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow n
: TITLE OF INVENTION: Virus and cassava vein mosaic virus
: FILE REFERENCE: 184332042
: CURRENT APPLICATION NUMBER: US/09/963.803
: CURRENT FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: FR 99/03925
: PRIOR FILING DATE: 1999-03-29
: PRIOR APPLICATION NUMBER: PCT IB00/00370
: PRIOR FILING DATE: 2000-10-05
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 7
: LENGTH: 301

```

```

RESULT 12
US-09-963-803-6
: Sequence 6, Application US/09963803
: GENERAL INFORMATION:
: APPLICANT: Meristem Therapeutics
: TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow n
: FILE REFERENCE: 184332042
: CURRENT APPLICATION NUMBER: US/09/963,803
: CURRENT FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: FR 99/03925
: PRIOR FILING DATE: 1999-03-29
: PRIOR APPLICATION NUMBER: PCT IB00/00370
: PRIOR FILING DATE: 2000-10-05
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 6

```

```

:      LENGTH: 398
:      TYPE: DNA
:      ORGANISM: Artificial Sequence
:      FEATURE:
:      OTHER INFORMATION: promoter Mp1147
:      FEATURE:
:      NAME/KEY: promoter
:      LOCATION: (1)..(398)
:      OTHER INFORMATION:
:      US-09-963-803-6

```

```

RESULT 13
PCT-US97-10376-1
; Sequence 1, Application PCT/US9710376
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: CASSAVA VEIN MOSAIC VIRUS PROMOTERS AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 36
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/us97/10376
; FILING DATE: 20-JUN-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/020.129
; FILING DATE: 20-JUN-1996
; INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;         LENGTH: 392 base pairs
;         TYPE: nucleic acid
;         STRANDEDNESS: single
;         TOPOLOGY: linear
;     MOLECULE TYPE: DNA (genomic)
;     HYPOTHEetical: NO
;     ANTI-SENSE: NO
; PCT-US97-10376-1

Query Match          20.1%, Score 120.6, DB 1, Length 392.
Best Local Similarity 93.3%, Pred. No. 4.9e+24;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      93 GAATTTTGAAGACCGTAACACTGACGACACAACAATAAAAGAAGAGATTAGGTGGTGAT 152
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      143 GAATTTTGAAGACGTAACCACTGACGACACAACATGAAGAAGAGATTAGGTGGTGAT 202

QY      153 TGTGAAGAAGACATAGAGACACATGTAAAGTGTGAATAATGTAAAGGCCGGAAGTAACCTT 212
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      203 TGTGAAGAAGACATAGAGACACATGTAAAGTGTGAATAATGTAAAGGCCGGAAGTAACCTT 262

QY      213 ATGCATTTGTATTT 227
        || | | | | |

```

; GENERAL INFORMATION:  
: APPLICANT: Verdaneur Bertrand

Search completed: April 14, 2003, 12:06:34  
Job time : 2423.62 secs



GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 08:19:51 ; Search time 475.052 Seconds  
(without alignments)  
5404.014 Million cell updates/sec

Title: US-09-963-803-22

Perfect score: 600  
Sequence: 1 aagctgcacgtcgtcagca.....cacacacactagagatcc 600

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 5824060 seqs, 2139321184 residues

Total number of hits satisfying chosen parameters: 11648120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_NA\_New:\*  
1: /cgn2\_6/pdata1/pna/PCT\_NEW\_COMB.seq:\*  
2: /cgn2\_6/pdata1/pna/US06\_NEW\_COMB.seq:\*  
3: /cgn2\_6/pdata1/pna/US07\_NEW\_COMB.seq:\*  
4: /cgn2\_6/pdata1/pna/US08\_NEW\_COMB.seq:\*  
5: /cgn2\_6/pdata1/pna/US09\_NEW\_COMB.seq:\*  
6: /cgn2\_6/pdata1/pna/US09\_NEW\_COMB.seq2:\*  
7: /cgn2\_6/pdata1/pna/US09\_NEW\_COMB.seq3:\*  
8: /cgn2\_6/pdata1/pna/US10\_NEW\_COMB.seq:\*  
9: /cgn2\_6/pdata1/pna/US10\_NEW\_COMB.seq2:\*  
10: /cgn2\_6/pdata1/pna/US60\_NEW\_COMB.seq:\*  
11: /cgn2\_6/pdata1/pna/US60\_NEW\_COMB.seq2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 120.6 | 20.1        | 532    | 6     | US-09-765-555A-1  |
| 2          | 120.6 | 20.1        | 838    | 6     | US-09-673-274B-19 |
| 3          | 120.6 | 20.1        | 1036   | 6     | US-09-673-274B-20 |
| 4          | 40.4  | 6.7         | 309    | 8     | US-10-380-935-30  |
| 5          | 40.4  | 6.7         | 532    | 8     | US-10-380-935-37  |
| 6          | 40.4  | 6.7         | 835    | 8     | US-10-391-414-10  |
| 7          | 40.4  | 6.7         | 1683   | 11    | US-60-434-166-147 |
| 8          | 40.4  | 6.7         | 2361   | 9     | US-10-302-267-1   |
| 9          | 40.4  | 6.7         | 3212   | 9     | US-10-130-150-13  |
| 10         | 40.4  | 6.7         | 3288   | 9     | US-10-130-150-18  |
| 11         | 40.4  | 6.7         | 3329   | 9     | US-10-130-150-15  |
| 12         | 40.4  | 6.7         | 5247   | 9     | US-10-160-764-40  |
| 13         | 40.4  | 6.7         | 5250   | 9     | US-10-160-764-4   |
| 14         | 40.4  | 6.7         | 5511   | 9     | US-10-160-764-48  |
| 15         | 40.4  | 6.7         | 5715   | 9     | US-10-160-764-52  |
| 16         | 40.4  | 6.7         | 5796   | 8     | US-10-378-810-2   |
| 17         | 40.4  | 6.7         | 6285   | 9     | US-10-160-764-42  |
| 18         | 40.4  | 6.7         | 6299   | 9     | US-10-160-764-50  |
| 19         | 40.4  | 6.7         | 8349   | 9     | US-10-198-478-16  |
| 20         | 40.4  | 6.7         | 10249  | 9     | US-10-198-478-14  |
| 21         | 40.4  | 6.7         | 10312  | 9     | US-10-198-478-15  |
| 22         | 40.4  | 6.7         | 10339  | 9     | US-10-198-478-13  |

|   |    |      |     |        |   |                     |                   |
|---|----|------|-----|--------|---|---------------------|-------------------|
| C | 23 | 40.4 | 6.7 | 13737  | 6 | US-09-538-414-10    | Sequence 10, Appl |
|   | 24 | 39.8 | 6.5 | 250715 | 7 | US-09-949-016-13294 | Sequence 9, Appl  |
|   | 25 | 38.8 | 6.5 | 206    | 9 | US-10-204-889-9     | Sequence 22, Appl |
|   | 26 | 38.8 | 6.5 | 382    | 1 | PCT-US02-17853-22   | Sequence 6, Appl  |
|   | 27 | 38.8 | 6.5 | 842    | 9 | US-10-321-434-6     | Sequence 11, Appl |
|   | 28 | 38.8 | 6.5 | 2267   | 1 | PCT-US02-17853-11   | Sequence 55, Appl |
|   | 29 | 38.8 | 6.5 | 2873   | 1 | PCT-US03-03435-55   | Sequence 38, Appl |
|   | 30 | 38.8 | 6.5 | 2873   | 9 | US-10-353-454-38    | Sequence 57, Appl |
|   | 31 | 38.8 | 6.5 | 2873   | 9 | US-10-356-088-55    | Sequence 48, Appl |
|   | 32 | 38.8 | 6.5 | 3002   | 9 | US-10-353-454-57    | Sequence 48, Appl |
|   | 33 | 38.8 | 6.5 | 3034   | 1 | PCT-US03-03435-48   | Sequence 31, Appl |
|   | 34 | 38.8 | 6.5 | 3034   | 9 | US-10-353-454-31    | Sequence 48, Appl |
|   | 35 | 38.8 | 6.5 | 3034   | 9 | US-10-356-088-48    | Sequence 57, Appl |
|   | 36 | 38.8 | 6.5 | 4182   | 5 | US-09-921-922A-7    | Sequence 6, Appl  |
|   | 37 | 38.8 | 6.5 | 5449   | 1 | PCT-US03-03435-57   | Sequence 7, Appl  |
|   | 38 | 38.8 | 6.5 | 5449   | 9 | US-10-353-454-40    | Sequence 40, Appl |
|   | 39 | 38.8 | 6.5 | 5449   | 9 | US-10-356-088-57    | Sequence 17, Appl |
|   | 40 | 38.8 | 6.5 | 6975   | 6 | US-09-464-528C-17   | Sequence 2, Appl  |
|   | 41 | 38.8 | 6.5 | 9555   | 5 | US-09-921-922A-6    | Sequence 7, Appl  |
|   | 42 | 38.8 | 6.5 | 13199  | 9 | US-10-137-125A-2    | Sequence 893, App |
|   | 43 | 38.8 | 6.5 | 17476  | 8 | US-10-385-446-7     | Sequence 113, App |
|   | 44 | 37   | 6.2 | 5195   | 9 | US-10-311-455-893   |                   |
|   | 45 | 37   | 6.2 | 6944   | 9 | US-10-311-506-113   |                   |

#### ALIGNMENTS

RESULT 1  
US-09-765-555A-1  
; Sequence 1, Application US/09765555A  
; GENERAL INFORMATION:  
; APPLICANT: The Scripps Research Institute  
; APPLICANT: Barbas, Carlos  
; APPLICANT: Stege, Justin  
; APPLICANT: Guan, Xueni  
; APPLICANT: Dalma, Bipin  
; TITLE OF INVENTION: Methods and compositions to modulate  
; FILE REFERENCE: 27801-20014.20  
; CURRENT APPLICATION NUMBER: US/09/765,555A  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: US/09/620,897  
; PRIOR FILING DATE: 2000-07-21  
; PRIOR APPLICATION NUMBER: US 60/177,468  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 532  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Promoter csmv  
US-09-765-555A-1

Query Match 20.1%; Score 120.6; DB 6; Length 532;  
Best local similarity 93.3%; Pred. No. 1.5e-25;  
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| QY | 93  | GAATATGAAAGCACTAGCACTGACGACAAACAAAGAAAGAAAGTAAGTGGCGAT  | 152 |
| DB | 231 | GAATCTTGAAGACCTAAGCACTGACGACAAACAAAGAAAGAAAGTAAGTGGCGAT | 290 |
| QY | 153 | TGTGAAGAGCAATAGAGGACACATGTAAGTGAAGTAAGGCGAAAGTAACCTT    | 212 |
| DB | 291 | TGTGAAGAGCAATAGAGGACACATGTAAGTGAAGTAAGGCGAAAGTAACCTT    | 350 |
| QY | 213 | ATGCATTGTGAATTT   | 227 |
| DB | 351 | ATCACAAGGAATCT  | 365 |

```

: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic oligonucleotide
: FEATURE:
: NAME/KEY: promoter
: LOCATION: (7)...(532)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (539)...(736)
: FEATURE:
: NAME/KEY: terminator
: LOCATION: (767)...(1030)
US-09-673-274B-20

Query Match          20.1%; Score 120.6; DB 6; Length 1036;
Best Local Similarity 93.3%; Pred. No. 1.9e-25;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 93 GAATTTGAGACGTAAACGACACTGACGACAAACAATGAAAAAGAAAGATTAAGTCGTCGAT 152
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 222 GAATTTGAGACGTAAACGACACTGACGACAAACAATGAAAAAGAAAGATTAAGTCGTCGAT 281
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 153 TGTGAAGAAGACATTAAGAGACACATGTAAGGTGAAAAATGTAAGGCGGAAAGTAACCTT 212
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 282 TGTGAAGAAGACATTAAGAGACACATGTAAGGTGAAAAATGTAAGGCGGAAAGTAACCTT 341
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 213 ATGCATTTGTAATTT 227
    || ||||| |
DB 342 ATCACCAANGAATCTT 356
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
US-10-380-935-30
: GENERAL INFORMATION:
: SEQUENCE 30, Application US/10380935
: ORGANISM:
: APPLICANT: WARNER, Simon, Anthony, James
: APPLICANT: HAWKES, Timothy, Robert
: TITLE OF INVENTION: HERBICIDE RESISTANT PLANTS
: FILE REFERENCE: PPD50594/MO
: CURRENT APPLICATION NUMBER: US/10/380,935
: PRIOR FILING DATE: 2003-03-19
: PRIOR APPLICATION NUMBER: GB0023911.1
: PRIOR FILING DATE: 2000-09-29
: PRIOR APPLICATION NUMBER: GB0027693.1
: PRIOR FILING DATE: 2000-11-13
: PRIOR APPLICATION NUMBER: GB0023910.3
: PRIOR FILING DATE: 2000-09-29
: NUMBER OF SEQ ID NOS: 70
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 30
: LENGTH: 309
: TYPE: DNA
: ORGANISM: Cauliflower Mosaic Virus
: FEATURE:
: OTHER INFORMATION: Enhancer
US-10-380-935-30

Query Match          6.7%; Score 40.4; DB 8; Length 309;
Best Local Similarity 88.0%; Pred. No. 0.073;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 396 GATTGATGTGATATCTCCACATGACGTAAAGGATGACGATGCCAGACTA 445
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 242 GATTGATGTGATATCTCCACATGACGTAAAGGATGACGATGCCAGACTA 291
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
US-10-380-935-37
: GENERAL INFORMATION:
: SEQUENCE 37, Application US/10380935
: ORGANISM:
: APPLICANT: WARNER, Simon, Anthony, James
: APPLICANT: HAWKES, Timothy, Robert

```



```
APPLICANT: ANDREWS, Christopher, John
: TITLE OF INVENTION: HERBICIDE RESISTANT PLANTS
: FILE REFERENCE: PPD50594/MO
: CURRENT APPLICATION NUMBER: US/10/380,935
: CURRENT FILING DATE: 2003-03-19
: PRIOR APPLICATION NUMBER: GB0023911.1
: PRIOR FILING DATE: 2000-09-29
: PRIOR APPLICATION NUMBER: GB0027693.1
: PRIOR FILING DATE: 2000-11-13
: PRIOR APPLICATION NUMBER: GB0023910.3
: PRIOR FILING DATE: 2000-09-29
: NUMBER OF SEQ ID NOS: 70
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 37
: LENGTH: 522
: TYPE: DNA
: ORGANISM: Pigwort Mosaic Virus
: FEATURE:
: OTHER INFORMATION: Enhancer
US-10-380-935-37
```

```
Query Match      6.7%; Score 40.4; DB 8; Length 522;
Best Local Similarity 88.0%; Pred. No. 0.085;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
OY      396 GATTGATGTGATATCTCCACTGACGTAGGCGATGCGCATGCCAGCAGCTA 445
Db      459 GATTGATGTGATATCTCCACTGACGTAGGCGATGCGCATGCCAGCAGCTA 508
```

```
RESULT 6
US-10-391-414-10
: Sequence 10, Application US/10391414
: GENERAL INFORMATION:
: APPLICANT: SHINOZAKI, Kazuko
: APPLICANT: KATSURA, Koji
: APPLICANT: ITO, Yusuke
: TITLE OF INVENTION: Stress Induced Promoter Derived From Rice
: FILE REFERENCE: 382.1041
: CURRENT APPLICATION NUMBER: US/10/391,414
: CURRENT FILING DATE: 2003-03-18
: PRIOR APPLICATION NUMBER: JP 2002-377316
: PRIOR FILING DATE: 2002-12-26
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 10
: LENGTH: 835
: TYPE: DNA
: ORGANISM: Cauliflower mosaic virus
US-10-391-414-10
```

```
Query Match      6.7%; Score 40.4; DB 8; Length 835;
Best Local Similarity 88.0%; Pred. No. 0.098;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
OY      258 GATTGATGTGATATCTCCACTGACGTAGGCGATGCGCATGCCAGCAGCTA 307
Db      729 GATTGATGTGATATCTCCACTGACGTAGGCGATGCGCATGCCAGCAGCTA 778
```

```
RESULT 7
US-60-434-166-147
: Sequence 147, Application US/60434166
: GENERAL INFORMATION:
: APPLICANT: Mendel Biotechnology
: APPLICANT: Creelman, Robert A.
: APPLICANT: Haake, Volker
: APPLICANT: Ratcliffe, Oliver
: APPLICANT: Heard, Jacqueline E.
: APPLICANT: Adam, Luc J.
: APPLICANT: Jiang, Cai-Zhong
: APPLICANT: Reuber, T. Lynne
: APPLICANT: Riechmann, Jose Luis
```

```
APPLICANT: Sherman, Bradley K.
: TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
: FILE REFERENCE: M81-0051 P
: CURRENT APPLICATION NUMBER: US/60/434,166
: CURRENT FILING DATE: 2002-12-17
: NUMBER OF SEQ ID NOS: 559
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 147
: LENGTH: 1683
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
: FEATURE:
: OTHER INFORMATION: G2227
US-60-434-166-147
```

```
Query Match      6.7%; Score 40.4; DB 11; Length 1683;
Best Local Similarity 88.0%; Pred. No. 0.12;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
OY      258 GATTGATGTGATATCTCCACTGACGTAGGCGATGCGCATGCCAGCAGCTA 307
Db      9      GATTGATGTGATATCTCCACTGACGTAGGCGATGCGCATGCCAGCAGCTA 58
```

```
RESULT 8
US-10-302-267-1
: Sequence 1, Application US/10302267
: GENERAL INFORMATION:
: APPLICANT: Keddie, James
: APPLICANT: Fromm, Michael
: APPLICANT: Heard, Jacqueline
: APPLICANT: Riechmann, Jose Luis
: APPLICANT: Adam, Luc
: APPLICANT: Biron, Pierie
: APPLICANT: Pineda, Omaira
: APPLICANT: Reuber, Lynne
: APPLICANT: Zhang, James
: APPLICANT: Yu, Guo-Liang
: APPLICANT: Jiang, Cai-Zhong
: APPLICANT: Samaha, Raymond
: APPLICANT: Pilgrim, Marsha
: APPLICANT: Creelman, Robert
: TITLE OF INVENTION: PLANT GENE SEQUENCES II
: FILE REFERENCE: M81-0007
: CURRENT APPLICATION NUMBER: US/10/302,267
: CURRENT FILING DATE: 2002-11-22
: PRIOR APPLICATION NUMBER: US/09/506,720
: PRIOR FILING DATE: 2000-02-17
: PRIOR APPLICATION NUMBER: 60/120,880
: PRIOR FILING DATE: 1999-02-18
: PRIOR APPLICATION NUMBER: 60/121,037
: PRIOR FILING DATE: 1999-02-22
: PRIOR APPLICATION NUMBER: 60/124,278
: PRIOR FILING DATE: 1999-03-11
: PRIOR APPLICATION NUMBER: 60/129,450
: PRIOR FILING DATE: 1999-04-15
: PRIOR APPLICATION NUMBER: 60/135,134
: PRIOR FILING DATE: 1999-05-20
: PRIOR APPLICATION NUMBER: 60/144,153
: PRIOR FILING DATE: 1999-07-15
: PRIOR APPLICATION NUMBER: 60/161,143
: PRIOR FILING DATE: 1999-10-22
: PRIOR APPLICATION NUMBER: 60/162,656
: PRIOR FILING DATE: 1999-11-01
: NUMBER OF SEQ ID NOS: 218
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 2361
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (144)..(2024)
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; OTHER INFORMATION: G274
US-10-302-267-1

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 9; Length 2361;
Best Local Similarity 88.0%; Pred. No. 0.13;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGTATATCTCCACTGACGTAAGGATGAGCATGCCAGCACTA 307
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DB 113 GATTGATGTATATCTCCACTGACGTAAGGATGAGCATGCCAGCACTA 162

RESULT 9
US-10-130-150-13
; Sequence 13, Application US/10130150
; GENERAL INFORMATION:
; APPLICANT: Shoseyov, Oded
; TITLE OF INVENTION: ASPERGILLUS NIGER BETA-GLUCOSIDASE GENE, PROTEIN AND USES THEREOF
; FILE REFERENCE: 02/23831
; CURRENT APPLICATION NUMBER: US/10/130,150
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 3212
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of recombinant construct expressing BglI protein
US-10-130-150-13

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 9; Length 3212;
Best Local Similarity 88.0%; Pred. No. 0.15;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGTATATCTCCACTGACGTAAGGATGAGCATGCCAGCACTA 307
      |||
DB 197 GATTGATGTATATCTCCACTGACGTAAGGATGAGCATGCCAGCACTA 246

RESULT 10
US-10-130-150-18
; Sequence 18, Application US/10130150
; GENERAL INFORMATION:
; APPLICANT: Shoseyov, Oded
; TITLE OF INVENTION: ASPERGILLUS NIGER BETA-GLUCOSIDASE GENE, PROTEIN AND USES THEREOF
; FILE REFERENCE: 02/23831
; CURRENT APPLICATION NUMBER: US/10/130,150
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 3288
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of recombinant construct expressing BglI protein fused
; OTHER INFORMATION: and ER retaining signal peptides
US-10-130-150-18

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 9; Length 3288;
Best Local Similarity 88.0%; Pred. No. 0.15;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGTATATCTCCACTGACGTAAGGATGAGCATGCCAGCACTA 307
      |||
DB 197 GATTGATGTATATCTCCACTGACGTAAGGATGAGCATGCCAGCACTA 246

RESULT 11
US-10-130-150-15
; Sequence 15, Application US/10130150
; GENERAL INFORMATION:

; APPLICANT: Shoseyov, Oded
; TITLE OF INVENTION: ASPERGILLUS NIGER BETA-GLUCOSIDASE GENE, PROTEIN AND USES THEREOF
; FILE REFERENCE: 02/23831
; CURRENT APPLICATION NUMBER: US/10/130,150
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 3329
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of recombinant construct expressing BglI protein fuse
; OTHER INFORMATION: signal peptide
US-10-130-150-15

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 9; Length 3329;
Best Local Similarity 88.0%; Pred. No. 0.15;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGTATATCTCCACTGACGTAAGGATGAGCATGCCAGCACTA 307
      |||
DB 197 GATTGATGTATATCTCCACTGACGTAAGGATGAGCATGCCAGCACTA 246

RESULT 12
US-10-160-764-40
; Sequence 40, Application US/10160764
; GENERAL INFORMATION:
; APPLICANT: Huang, Yafan
; APPLICANT: Chailifoux, Maryse
; APPLICANT: Wang, Yang
; APPLICANT: Kuzma, Monika Maria
; APPLICANT: Gille, Angela Patricia
; TITLE OF INVENTION: Compositions and Methods of Increasing Stress Tolerance
; TITLE OF INVENTION: In Plants
; FILE REFERENCE: 22542-008
; CURRENT APPLICATION NUMBER: US/10/160,764
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,766
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/348,909
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 5247
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequence: Plasmid
; OTHER INFORMATION: pBI121-35S-AtPTA
US-10-160-764-40

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 9; Length 5247;
Best Local Similarity 88.0%; Pred. No. 0.17;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 GATTGATGTATATCTCCACTGACGTAAGGATGAGCATGCCAGCACTA 307
      |||
DB 3209 GATTGATGTATATCTCCACTGACGTAAGGATGAGCATGCCAGCACTA 3258

RESULT 13
US-10-160-764-4
; Sequence 4, Application US/10160764
; GENERAL INFORMATION:
; APPLICANT: Huang, Yafan
; APPLICANT: Chailifoux, Maryse
; APPLICANT: Wang, Yang
; APPLICANT: Kuzma, Monika Maria
; APPLICANT: Gille, Angela Patricia
; TITLE OF INVENTION: Compositions and Methods of Increasing Stress Tolerance
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; TITLE OF INVENTION: in Plants
; FILE REFERENCE: 22542-008
; CURRENT APPLICATION NUMBER: US/10/160,764
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,766
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/348,909
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 5250
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
US-10-160-764-4

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 9; Length 5250;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 258 GATTGATGTGATATCTCCACTGACGTAGGAGTACGCGATGCCAGACTA 307
Db 3209 GATTGATGTGATATCTCCACTGACGTAGGAGTACGCGACCAATCCCACTA 3258

RESULT 14
US-10-160-764-48
; Sequence 48, Application US/10160764
; GENERAL INFORMATION:
; APPLICANT: Huang, Yafan
; APPLICANT: Chailloux, Maryse
; APPLICANT: Wang, Yang
; APPLICANT: Kuzma, Monika Maria
; APPLICANT: Gilley, Angela Patricia
; TITLE OF INVENTION: Compositions and Methods of Increasing Stress Tolerance
; TITLE OF INVENTION: in Plants
; FILE REFERENCE: 22542-008
; CURRENT APPLICATION NUMBER: US/10/160,764
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,766
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/348,909
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 5511
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
US-10-160-764-48

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 9; Length 5511;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 258 GATTGATGTGATATCTCCACTGACGTAGGAGTACGCGATGCCAGACTA 307
Db 3209 GATTGATGTGATATCTCCACTGACGTAGGAGTACGCGACCAATCCCACTA 3258

RESULT 15
US-10-160-764-52
; Sequence 52, Application US/10160764
; GENERAL INFORMATION:
; APPLICANT: Huang, Yafan
; APPLICANT: Chailloux, Maryse
; APPLICANT: Wang, Yang
```

```
; APPLICANT: Kuzma, Monika Maria
; APPLICANT: Gilley, Angela Patricia
; TITLE OF INVENTION: Compositions and Methods of Increasing Stress Tolerance
; TITLE OF INVENTION: in Plants
; FILE REFERENCE: 22542-008
; CURRENT APPLICATION NUMBER: US/10/160,764
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,766
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/348,909
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 5715
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
US-10-160-764-52

Query Match
Best Local Similarity 6.7%; Score 40.4; DB 9; Length 5715;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 258 GATTGATGTGATATCTCCACTGACGTAGGAGTACGCGATGCCAGACTA 307
Db 3209 GATTGATGTGATATCTCCACTGACGTAGGAGTACGCGACCAATCCCACTA 3258
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Search completed: April 14, 2003, 12:27:55  
Job time : 490.052 secs



GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 06:53:52 : Search time 1394.64 Seconds  
(without alignments)  
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Title: US-09-963-803-22

Perfect score: 600  
Sequence: 1 aagcttgcatgcctgcagca.....cacacacactagagatcc 600

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vtc:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1          | 43.8  | 7.3         | 224    | 17    | BH746858    |
| 2          | 42.4  | 7.1         | 561    | 13    | BM162517    |
| 3          | 41.8  | 7.0         | 1101   | 17    | CNS00396    |
| 4          | 41    | 6.8         | 222    | 13    | BM161725    |
| 5          | 40.4  | 6.7         | 112    | 17    | BH751161    |
| 6          | 40.4  | 6.7         | 142    | 17    | BH749349    |

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| C | 7  | 40.4 | 6.7 | 153 | 17 | BH619283 | BH619283 | SALK_0407  |
| C | 8  | 40.4 | 6.7 | 158 | 17 | BH747013 | BH747013 | SALK_0080  |
| C | 9  | 40.4 | 6.7 | 153 | 17 | BH748291 | BH748291 | SALK_0451  |
| C | 10 | 40.4 | 6.7 | 165 | 17 | BH747357 | BH747357 | SALK_0165  |
| C | 11 | 40.4 | 6.7 | 175 | 17 | BH746616 | BH746616 | SALK_0452  |
| C | 12 | 40.4 | 6.7 | 177 | 17 | BH802465 | BH802465 | SALK_0193  |
| C | 13 | 40.4 | 6.7 | 190 | 17 | BH752801 | BH752801 | SALK_0193  |
| C | 14 | 40.4 | 6.7 | 193 | 17 | BH748289 | BH748289 | SALK_0450  |
| C | 15 | 40.4 | 6.7 | 214 | 17 | BH747829 | BH747829 | SALK_0353  |
| C | 16 | 40.4 | 6.7 | 215 | 17 | BH753813 | BH753813 | SALK_0296  |
| C | 17 | 40.4 | 6.7 | 219 | 17 | BH747744 | BH747744 | SALK_0337  |
| C | 18 | 40.4 | 6.7 | 220 | 17 | BH747438 | BH747438 | SALK_0174  |
| C | 19 | 40.4 | 6.7 | 221 | 17 | BH802415 | BH802415 | SALK_0260  |
| C | 20 | 40.4 | 6.7 | 230 | 17 | BH746474 | BH746474 | SALK_0428  |
| C | 21 | 40.4 | 6.7 | 230 | 17 | BH799173 | BH799173 | SALK_02581 |
| C | 22 | 40.4 | 6.7 | 237 | 17 | BH802463 | BH802463 | SALK_0260  |
| C | 23 | 40.4 | 6.7 | 244 | 17 | BH746375 | BH746375 | SALK_0402  |
| C | 24 | 40.4 | 6.7 | 248 | 17 | BH254798 | BH254798 | SALK_0172  |
| C | 25 | 40.4 | 6.7 | 251 | 17 | BH750171 | BH750171 | SALK_0371  |
| C | 26 | 40.4 | 6.7 | 254 | 17 | BH748500 | BH748500 | SALK_0460  |
| C | 27 | 40.4 | 6.7 | 256 | 17 | BH748499 | BH748499 | SALK_0460  |
| C | 28 | 40.4 | 6.7 | 258 | 17 | BH802470 | BH802470 | SALK_0260  |
| C | 29 | 40.4 | 6.7 | 261 | 17 | BH802493 | BH802493 | SALK_0318  |
| C | 30 | 40.4 | 6.7 | 268 | 17 | BH611919 | BH611919 | SALK_0064  |
| C | 31 | 40.4 | 6.7 | 269 | 17 | BH211646 | BH211646 | SALK_0064  |
| C | 32 | 40.4 | 6.7 | 269 | 17 | BH802489 | BH802489 | SALK_0260  |
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| C | 34 | 40.4 | 6.7 | 272 | 17 | BH802428 | BH802428 | SALK_0260  |
| C | 35 | 40.4 | 6.7 | 274 | 17 | BH802495 | BH802495 | SALK_0260  |
| C | 36 | 40.4 | 6.7 | 279 | 17 | BH748475 | BH748475 | SALK_0460  |
| C | 37 | 40.4 | 6.7 | 281 | 17 | BH750170 | BH750170 | SALK_0371  |
| C | 38 | 40.4 | 6.7 | 281 | 17 | BH802443 | BH802443 | SALK_0260  |
| C | 39 | 40.4 | 6.7 | 284 | 17 | BH213307 | BH213307 | SALK_0090  |
| C | 40 | 40.4 | 6.7 | 284 | 17 | BH746665 | BH746665 | SALK_0457  |
| C | 41 | 40.4 | 6.7 | 286 | 17 | BH747007 | BH747007 | SALK_0078  |
| C | 42 | 40.4 | 6.7 | 293 | 17 | BH610310 | BH610310 | SALK_0085  |
| C | 43 | 40.4 | 6.7 | 296 | 17 | BH213532 | BH213532 | SALK_0093  |
| C | 44 | 40.4 | 6.7 | 335 | 17 | BH213230 | BH213230 | SALK_0089  |
| C | 45 | 40.4 | 6.7 | 344 | 17 | BH747662 | BH747662 | SALK_0323  |

## ALIGNMENTS

RESULT 1  
BH746858  
LOCUS  
DEFINITION  
224 bp DNA linear GSS 27-FEB-2002  
SALK\_003694.51.40.x Arabidopsis thaliana genomic clone SALK\_003694.51.40.x, DNA  
Arabidopsis thaliana genomic clone SALK\_003694.51.40.x, DNA  
sequence.

ACCESSION  
BH746858  
VERSION  
BH746858.1  
KEYWORDS  
GSS.

ORGANISM  
thale cress.  
Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
1 (bases 1 to 224)  
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,  
C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Predans,L., Shinn,P.,  
Zimmerman,J., and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
Unpublished (2001)

CONTACT: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies (SIGAL)  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: eckersalk.edu

This is single pass sequence recovered from the left border of

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1..561
/organism="Plasmodium yoelli yoelli"
/strain="17XL"
/db_xref="taxon:73239"
/clone="P1CK164"
/clone_1fb="PyBS"
/dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/notes="vector: pMD-GAL4. At 20-25% parasitemia, blood was
collected from BALB/cBY mice infected with P17XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose columns. Total RNA was
isolated using the guanidinium isothiocyanate method, and
RNA isolated using oligo(dT)-cellulose chromatography."

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FEATURES
    source
        1..1101
            /organism="Drosophila melanogaster"
            /db_xref="taxon:7227"
            /clone="BACR08K10"
            /clone_1db="RPC1-98"
            /note="end : TET3"

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| BASE COUNT            | 201 a   | 64 c   | 131 g | 202 t  | 503 others      |  |  |
| ORIGIN                |   |  |       |        |                 |  |  |
| Query Match           | 7.0%; Score 41.8; DB 17; Length 1101;   |  |       |        |                 |  |  |
| Best Local Similarity | 17.3%; Pred. No. 1.7;   |  |       |        |                 |  |  |
| Matches               | Conservative 107; Mismatches 79; Indels 0; Gaps 0;  |  |       |        |                 |  |  |
| Oy                    | 118   | GACACAAATGAAAAGACAGATAAAGTCGGTGTATTGGAAGAACAATAGACACACAT   | 177   |        |                 |  |  |
| Db                    | 758   | RWADRTDRDDDDDDRDAGRGKRWRRTRWRKMRKRDPTRDMDADADDARDRRRRR     | 699   |        |                 |  |  |
| Oy                    | 178   | GTAAGGTGGAANAATGTAGAGCGCGGAACCTATCATTTTGTAATTTGGTTACACT    | 237   |        |                 |  |  |
| Db                    | 698   | GADGKGKKTKRRRRRRRRATWDRTDAMWADAMWTTDTDDTDKDRRKGRARRRR      | 639   |        |                 |  |  |
| Oy                    | 238   | AGTGATGATGTATATCAAGATTGATGTATATCCACGTACAGTAAAGTGACGCAT     | 297   |        |                 |  |  |
| Db                    | 638   | TTPARAOWMTWTWKAMDMAKMKPTFADWDMDNADWTWTDARKADDMAKARAWRRRORA | 579   |        |                 |  |  |
| Oy                    | 298   | GCCACGACTACTGATGTGATGTGATATCAAGATTGATGTGATATCT             | 342   |        |                 |  |  |
| Db                    | 578   | RAARADRMTTKGKTITTTATTTWAAFAAMWAMAATTTATWTTT                | 534   |        |                 |  |  |
| <hr/>                 |   |  |       |        |                 |  |  |
| RESULT 4              |   |  |       |        |                 |  |  |
| BM161725              |   |  |       |        |                 |  |  |
| LOCUS                 | BM161725  | 222 bp   | mRNA  | linear | EST 04-DEC-2001 |  |  |
| DEFINITION            | E57564248 PYBS Plasmodium yoelli yoelli cDNA clone pyCKI31 5' end,  |  |       |        |                 |  |  |
| ACCESSION             | BM161725  |  |       |        |                 |  |  |
| VERSION               | BM161725.1 GI:17307406  |  |       |        |                 |  |  |
| KEYWORDS              | EST.  |  |       |        |                 |  |  |
| SOURCE                | Plasmodium yoelli yoelli.   |  |       |        |                 |  |  |
| ORGANISM              | Eukaryote; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  |  |       |        |                 |  |  |
| REFERENCE             | 1 (bases 1 to 222)  |  |       |        |                 |  |  |
| AUTHORS               | Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B., Fraser,C.M. and Carucci,D.J.   |  |       |        |                 |  |  |
| TITLE                 | Plasmodium yoelli EST project at TIGR   |  |       |        |                 |  |  |
| JOURNAL               | Unpublished (2001)  |  |       |        |                 |  |  |
| COMMENT               | Contact: Jane Carlton<br>Parasite Genomics Group<br>The Institute for Genomic Research<br>9712 Medical Center Drive, Rockville, MD 20850, USA<br>Tel: 301-530-9319<br>Fax: 301-838-0208<br>Email: carlton@tigr.org<br>For clone info, please contact the Malaria Research and Reference Reagent Resource Center, ATCC<br><a href="http://www.malaria.mr4.org/mr4pages/index.html">http://www.malaria.mr4.org/mr4pages/index.html</a><br>Seq primer: ADF.<br>Location/Qualifiers<br>1..222<br>/organism="Plasmodium yoelli yoelli"<br>/strain="17XL"<br>/db_xref="taxon:73239"<br>/clone="pyCKI31"<br>/_clone_1lb="PYBS"<br>/dev_stage="asexual blood stages"<br>/lab_host="E. coli XL-1 Blue"<br>/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose columns. Total RNA was isolated using the guanidium thiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to |  |       |        |                 |  |  |

| BASE COUNT            | 99 a   | 25 c | 38 g | 60 t |
|-----------------------|--|------|------|------|
| ORIGIN                |  |      |      |      |
| Query Match           | 6.8%; Score 41; DB 13; Length 222;   |      |      |      |
| Best Local Similarity | 53.4%; Pred. No. 2.2;  |      |      |      |
| Matches               | 86; Conservative 0; Mismatches 75; Indels 0; Gaps 0;   |      |      |      |
| QY                    | 88 TGTGGATTATTGAGACGTAAAGCACTGACGCAACATGMAAAGACATAGTCG 147   |      |      |      |
| Db                    | 10 TGTAAAGATGATGATATATATATACAAACAACATCGCTGAAATATACGCAAAATCG 69   |      |      |      |
| QY                    | 148 GTGATTGTGAAGAAGACATAGACACACATGATGAGGTGGAATAATGATGAGCGGCAAACTA 207  |      |      |      |
| Db                    | 70 GAATTATGAAAAATGCGCTACAGGTACATATAAATGATAGAAATCAACAAAGTCGAATGAA 129   |      |      |      |
| QY                    | 208 ACCTTATGCATTGTAAATTTGGTTACGACATGATGATGATG 248  |      |      |      |
| Db                    | 130 GCGCGAAGCAATCATATATATATTTATTTATGCTTATTTATG 170   |      |      |      |
| RESULT 5              |  |      |      |      |
| LOCUS                 | BH751161   |      |      |      |
| DEFINITION            | BH751161 112 bp DNA linear GSS 27-FEB-2002   |      |      |      |
| ACCESSION             | SALK_049464.49.75.x Arabidopsis thaliana TDNA insertion lines  |      |      |      |
| VERSION               | BH751161   |      |      |      |
| KEYWORDS              | Arabidopsis thaliana genomic clone SALK_049464.49.75.x, DNA sequence.  |      |      |      |
| SOURCE                | GSS.   |      |      |      |
| ORGANISM              | thale cress.   |      |      |      |
| REFERENCE             | Arabidopsis thaliana   |      |      |      |
| AUTHORS               | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 112)  |      |      |      |
| TITLE                 | Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab , C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.   |      |      |      |
| JOURNAL               | A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  |      |      |      |
| COMMENT               | Contact: Joseph R. Ecker<br>Salk Institute Genomic Analysis Laboratory (SIGMAL)<br>The Salk Institute for Biological Studies<br>10010 N. Torrey Pines Road, La Jolla, CA 92037, USA<br>Tel: 858 453 4100 x1752<br>Fax: 858 558 6379<br>Email: eckeresalk.edu   |      |      |      |
| FEATURES              | This is single pass sequence recovered from the left border of TDNA.   |      |      |      |
| source                | Class: TDNA tagged.  |      |      |      |
|                       | Location/Qualifiers  |      |      |      |
|                       | 1..112   |      |      |      |
|                       | /organism="Arabidopsis thaliana"   |      |      |      |
|                       | /strain="Columbia 0"   |      |      |      |
|                       | /dd_xref="taxon:3702"  |      |      |      |
|                       | /clone="SALK_049464.49.75.x"   |      |      |      |
|                       | /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at <a href="http://signal.salk.edu/tdna_protocols.html">http://signal.salk.edu/tdna_protocols.html</a> " |      |      |      |
| BASE COUNT            | 31 a   | 26 c | 25 g | 30 t |
| ORIGIN                |  |      |      |      |
| Query Match           | 6.7%; Score 40.4; DB 17; Length 112;   |      |      |      |
| Best Local Similarity | 88.0%; Pred. No. 2.9;  |      |      |      |

Matches 44: Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 396 GATTGATGATATCTCCAGCTGACGTAAGGATGACGATGCACAGACTA 445  
 ||||||||||||||||||||||||||||||||||||||| 1 |||||  
 Db 3 GATTGATGATATCTCCAGCTGACGTAAGGATGACGCAATCCCACTA 52

RESULT 6  
 LOCUS BH749349 142 bp DNA linear GSS 27-FEB-2002  
 DEFINITION SALK\_047736.48.15.x Arabidopsis thaliana TDNA insertion lines  
 sequence.  
 Arabidopsis thaliana genomic clone SALK\_047736.48.15.x, DNA  
 accession  
 BH749349  
 VERSION BH749349.1 GI:18964144  
 KEYWORDS GSS.  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 142)  
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab  
 ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.  
 , Zimmerman,J., and Ecker,J.R.  
 A Sequence-Indexed Library of Insertion Mutations in the  
 Arabidopsis Genome  
 Unpublished (2001)  
 Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: eckere@salk.edu  
 This is single pass sequence recovered from the left border of  
 TDNA.  
 Class: TDNA tagged.  
 Location/Qualifiers  
 1..142  
 /organism="Arabidopsis thaliana"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_047736.48.15.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

BASE COUNT 41 a 36 c 30 g 35 t

ORIGIN

Query Match 6.7%; Score 40.4; DB 17; Length 142;  
 Best Local Similarity 88.0%; Pred. No. 3;  
 Matches 44: Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 396 GATTGATGATATCTCCAGCTGACGTAAGGATGACGATGCACAGACTA 445  
 ||||||||||||||||||||||||||||||||||||||| 1 |||||  
 Db 33 GATTGATGATATCTCCAGCTGACGTAAGGATGACGCAATCCCACTA 82

RESULT 7  
 LOCUS BH619283 153 bp DNA linear GSS 30-JAN-2002  
 DEFINITION SALK\_040762 Arabidopsis thaliana TDNA insertion lines Arabidopsis  
 thaliana genomic clone SALK\_040762, DNA sequence.  
 accession  
 BH619283  
 VERSION BH619283.1 GI:18429799  
 KEYWORDS GSS.  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 153)  
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab  
 ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.  
 , Zimmerman,J., and Ecker,J.R.  
 A Sequence-Indexed Library of Insertion Mutations in the  
 Arabidopsis Genome  
 Unpublished (2001)  
 Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: eckere@salk.edu  
 This is single pass sequence recovered from the left border of  
 TDNA.  
 Class: TDNA tagged.  
 Location/Qualifiers  
 1..153  
 /organism="Arabidopsis thaliana"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_040762"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

BASE COUNT 36 a 34 c 36 g 47 t

ORIGIN

Query Match 6.7%; Score 40.4; DB 17; Length 153;  
 Best Local Similarity 88.0%; Pred. No. 3;  
 Matches 44: Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 396 GATTGATGATATCTCCAGCTGACGTAAGGATGACGATGCACAGACTA 445  
 ||||||||||||||||||||||||||||||||||||||| 1 |||||  
 Db 110 GATTGATGATATCTCCAGCTGACGTAAGGATGACGCAATCCCACTA 61

RESULT 8  
 LOCUS BH747013 153 bp DNA linear GSS 27-FEB-2002  
 DEFINITION SALK\_008070.43.05.x Arabidopsis thaliana TDNA insertion lines  
 sequence.  
 Arabidopsis thaliana genomic clone SALK\_008070.43.05.x, DNA  
 accession  
 BH747013  
 VERSION BH747013.1 GI:18960128  
 KEYWORDS GSS.  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 153)  
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab  
 ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.  
 , Zimmerman,J., and Ecker,J.R.  
 A Sequence-Indexed Library of Insertion Mutations in the  
 Arabidopsis Genome  
 Unpublished (2001)  
 Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: eckere@salk.edu



This is single pass sequence recovered from the left border of TDNA.

FEATURES  
source

Class: TDNA tagged.  
Location/Qualifiers  
1. 153  
/organism="Arabidopsis thaliana"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_008070.43.05.x"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

BASE COUNT 47 a 37 c 33 g 36 t

ORIGIN

Query Match 6.7%; Score 40.4; DB 17; Length 153;  
Best Local Similarity 88.0%; Pred. No. 3;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 396 GATTGATGTGATATCTCCACTGACGTAGGATGACGATCCACGACTA 445  
|||||  
Db 44 GATTGATGTGATATCTCCACTGACGTAGGATGACGATCCACGACTA 93

RESULT 9  
BH748291 158 bp DNA linear GSS 27-FEB-2002  
LOCUS SALK\_045100.51.10.x Arabidopsis thaliana TDNA insertion lines  
DEFINITION Arabidopsis thaliana genomic clone SALK\_045100.51.10.x, DNA sequence.

ACCESSION BH748291  
VERSION BH748291.1 GI:18961648  
KEYWORDS GSS.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1 (bases 1 to 158)

AUTHORS

Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrihab ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.  
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

Unpublished (2001)

JOURNAL  
COMMENT

Salk Institute Genomic Analysis Laboratory (SIGNAL)  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: eckersalk.edu

This is single pass sequence recovered from the left border of TDNA.  
Class: TDNA tagged.  
Location/Qualifiers  
1. 158  
/organism="Arabidopsis thaliana"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_045100.51.10.x"

FEATURES  
source

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

BASE COUNT 37 a 35 c 37 g 49 t

ORIGIN

Query Match 6.7%; Score 40.4; DB 17; Length 158;  
Best Local Similarity 88.0%; Pred. No. 3;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 396 GATTGATGTGATATCTCCACTGACGTAGGATGACGATCCACGACTA 445  
|||||  
Db 110 GATTGATGTGATATCTCCACTGACGTAGGATGACGATCCACGACTA 61

RESULT 10  
BH747357 165 bp DNA linear GSS 27-FEB-2002  
LOCUS SALK\_016522.55.50.x Arabidopsis thaliana TDNA insertion lines  
DEFINITION Arabidopsis thaliana genomic clone SALK\_016522.55.50.x, DNA sequence.

ACCESSION BH747357  
VERSION BH747357.1 GI:18960472  
KEYWORDS GSS.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1 (bases 1 to 165)

AUTHORS

Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrihab ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.  
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL  
COMMENT

Salk Institute Genomic Analysis Laboratory (SIGNAL)  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: eckersalk.edu

This is single pass sequence recovered from the left border of TDNA.  
Class: TDNA tagged.  
Location/Qualifiers  
1. 165  
/organism="Arabidopsis thaliana"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_016522.55.50.x"

FEATURES  
source

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

BASE COUNT 45 a 43 c 39 g 38 t

Query Match 6.7%; Score 40.4; DB 17; Length 165;  
Best Local Similarity 88.0%; Pred. No. 3;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 396 GATTGATGTGATATCTCCACTGACGTAGGATGACGATCCACGACTA 445  
|||||  
Db 34 GATTGATGTGATATCTCCACTGACGTAGGATGACGATCCACGACTA 83

RESULT 11  
BH746616 175 bp DNA linear GSS 27-FEB-2002  
LOCUS SALK\_045268.54.50.x Arabidopsis thaliana TDNA insertion lines  
DEFINITION Arabidopsis thaliana genomic clone SALK\_045268.54.50.x, DNA sequence.

ACCESSION BH746616 GI:18959731  
 VERSION BH746616.1  
 KEYWORDS GSS.  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 175)  
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadlinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J., and Ecker,J.R.  
 A Sequence-indexed Library of Insertion Mutations in the Arabidopsis Genome  
 Unpublished (2001)  
 Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: eckers@salk.edu  
 This is single pass sequence recovered from the left border of TDNA.  
 Class: TDNA tagged.  
 Location/Qualifiers  
 1..175  
 /organism="Arabidopsis thaliana"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_045268.54.50.x"  
 /clone\_1lb="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at <http://signal.salk.edu/tdna-protocols.html>"  
 BASE COUNT 54 a 43 c 40 g 38 t  
 ORIGIN  
 Query Match 6.7%; Score 40.4; DB 17; Length 175;  
 Best Local Similarity 88.0%; Pred. No. 3;  
 Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 396 GATTGATGATATCTCCACTGACGTAAGGATGACGATCCACGACTA 445  
 |||||||||||||||||||||||||||||||||||||||  
 Db 66 GATTGATGATATCTCCACTGACGTAAGGATGACGATCCACGACTA 115  
 RESULT 12  
 BH802465 177 bp DNA linear GSS 25-APR-2002  
 LOCUS 1008026F10.y2 1008 - Rescuemu Grid I Zea mays genomic, DNA  
 DEFINITION  
 sequence.  
 ACCESSION BH802465  
 VERSION BH802465.1 GI:20316614  
 KEYWORDS GSS.  
 SOURCE Zea mays.  
 ORGANISM Zea mays.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 177)  
 Walbot,V.  
 Maize genomic sequences found using engineered Rescuemu transposon  
 Unpublished (2001)  
 Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Email: walbot@stanford.edu  
 Very probable ligation site found so sequence was trimmed.  
 Post-ligation sequence submitted separately.  
 Plate: 1008026 row: 10  
 Class: transposon-tagged  
 Location/Qualifiers  
 1..177  
 /organism="Zea mays"  
 /cultivar="mixed background W23/A188/B73"  
 /db\_xref="taxon:4577"  
 /clone\_1lb="1008 Rescuemu Grid I"  
 /issue\_type="leaf"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /note="Organ: leaf; Vector: Rescuemu (engineered from pluescript backbone); Site\_1: BamHI; Site\_2: BglII; Rescuemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuemu, go to the web site [www.zmmb.jastate.edu](http://www.zmmb.jastate.edu) and follow the links for 'Rescuemu.' Grid I was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."  
 BASE COUNT 39 a 38 c 47 g 53 t  
 ORIGIN  
 Query Match 6.7%; Score 40.4; DB 17; Length 177;  
 Best Local Similarity 88.0%; Pred. No. 3;  
 Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 327 GATTGATGATATCTCCACTGACGTAAGGATGACGATCCACGACTA 376.  
 |||||||||||||||||||||||||||||||||||||||  
 Db 118 GATTGATGATATCTCCACTGACGTAAGGATGACGATCCACGACTA 69  
 RESULT 13  
 BH752801 190 bp DNA linear GSS 27-FEB-2002  
 LOCUS SALK\_019366.54.25.x Arabidopsis thaliana TDNA insertion lines  
 DEFINITION  
 Arabidopsis thaliana genomic clone SALK\_019366.54.25.x, DNA sequence.  
 ACCESSION BH752801  
 VERSION BH752801.1 GI:18972023  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 190)  
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadlinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J., and Ecker,J.R.  
 A Sequence-indexed Library of Insertion Mutations in the Arabidopsis Genome  
 Unpublished (2001)  
 Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: eckers@salk.edu  
 This is single pass sequence recovered from the left border of TDNA.  
 Class: TDNA tagged.  
 Location/Qualifiers  
 1..190  
 /organism="Arabidopsis thaliana"  
 /strain="Columbia 0"  
 FEATURES  
 source

/db\_xref="taxon:3702"  
/clone="SALK\_019366.54.25.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

BASE COUNT 52 a 52 c 41 g 45 t

ORIGIN

Query Match 6.7%; Score 40.4; DB 17; Length 190;  
Best Local Similarity 88.0%; Pred. No. 3.1;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 396 GATTGATGATATCTCCACTGACGTAGGAGATGCCACGACTA 445  
|||||  
DB 81 GATTGATGATATCTCCACTGACGTAGGAGATGCCACGACTA 130  
|||||

RESULT 14  
BH748289 193 bp DNA linear GSS 27-FEB-2002  
LOCUS SALK\_045097.54.25.x Arabidopsis thaliana TDNA insertion lines  
DEFINITION Arabidopsis thaliana genomic clone SALK\_045097.54.25.x. DNA  
sequence.  
ACCESSION BH748289  
VERSION BH748289.1 GI:18961643  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana  
ORGANISM thale cress.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 193)  
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadriab,  
C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,  
Zimmerman,J. and Ecker,J.R.  
A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
Unpublished (2001)  
CONTACT: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of  
TDNA.  
Class: TDNA tagged.  
Location/Qualifiers  
1..193  
/organism="Arabidopsis thaliana"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_045097.54.25.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

BASE COUNT 61 a 48 c 43 g 41 t

ORIGIN

Query Match 6.7%; Score 40.4; DB 17; Length 193;  
Best Local Similarity 88.0%; Pred. No. 3.1;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 396 GATTGATGATATCTCCACTGACGTAGGAGATGCCACGACTA 445

|||||  
DB 84 GATTGATGATATCTCCACTGACGTAGGAGATGCCACGACTA 133  
|||||

RESULT 15  
BH747829 214 bp DNA linear GSS 27-FEB-2002  
LOCUS SALK\_035354.55.75.x Arabidopsis thaliana TDNA insertion lines  
DEFINITION Arabidopsis thaliana genomic clone SALK\_035354.55.75.x. DNA  
sequence.  
ACCESSION BH747829  
VERSION BH747829.1 GI:18960944  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana  
ORGANISM thale cress.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 214)  
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadriab,  
C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,  
Zimmerman,J. and Ecker,J.R.  
A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
Unpublished (2001)  
CONTACT: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of  
TDNA.  
Class: TDNA tagged.  
Location/Qualifiers  
1..214  
/organism="Arabidopsis thaliana"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_035354.55.75.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

BASE COUNT 58 a 56 c 52 g 48 t

ORIGIN

Query Match 6.7%; Score 40.4; DB 17; Length 214;  
Best Local Similarity 88.0%; Pred. No. 3.1;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 396 GATTGATGATATCTCCACTGACGTAGGAGATGCCACGACTA 445  
|||||  
DB 104 GATTGATGATATCTCCACTGACGTAGGAGATGCCACGACTA 153  
|||||

Search completed: April 14, 2003, 10:25:46  
Job time : 1396.64 secs

